

Fig. 1.

Sequence ID 1

1    TGCG AGG GGT GCA AGG AGT TCT TCA GGC GGA GTG TAA CCA AAA ATG  
      ACGC TCC CCA CGT TCC TCA AGA AGT CCG CCT CAC ATT GGT TTT TAC

46    CAG TGT ACA TAT GCA AAT TCG GCC ATG CTT GCG AAA TGG ATA TGT  
      GTC ACA TGT ATA CGT TTA AGC CGG TAC GAA CGC TTT ACC TAT ACA

91    ATA TGC GGA GAA AAT GCC AAG AGT A  
      TAT ACG CCT CTT TTA CGG TTC TCA T

Sequence ID 2  
**Fig.2.**

3	9	15	21	27	33	39	45										
1	TCC	ACT	GGT	GTT	ACC	ACA	AAG	GAA	AAC	ATC	TCC	TGT	GCC	TCT	GCT	CAT	TTA
	AGG	TGA	CCA	CAA	AAG	TGG	TGG	TGT	CTT	TTC	CGG	AGA	CGA	GTA	CGA	GTA	AAT
46	GAG	GGT	GGT	GCT	AAG	AAG	GTC	ATC	ATC	TCC	TGC	TGC	CCA	GCG	CTG		
	CTC	CCA	CCA	CGA	TTC	TTC	CAG	TAG	TAG	AGG	ACG	ACG	GGT	CGC	GAC		
91	ACC	CAT	GTT	CGT	CGT	TGG	TGG	CAA	CCT	TGA	AGC	AGT	ATG	ACC	CCT		
	TGG	GTA	CAA	GCA	GCA	ACC	ACA	GTT	GGA	ACT	TCG	TCA	TAC	TGG	GGA		
136	CTT	ACA	AGG	TCA	TCT	CCA	ACG	CCT	CCT	GCA	CAA	CCA	ACT	GCC	TCG		
	GAA	TGT	TCC	AGT	AGA	GGT	TGC	GGA	GGA	CGT	GTT	GGT	TGA	CGG	AGC		
181	CTC	CTC	TCG	CTA	AGG	TCA	TCC	ATG	ACA	ACT	TCG	AGA	TCA	TTG	AAG		
	GAG	GAG	GAG	GAT	TCC	AGT	AGG	TAC	TGT	TGA	AGC	TCT	AGT	AAC	TTC		
226	GTC	TGA	TGA	CCA	CTG	TAC	ACG	CCA	CCA	CTG	CCA	CCC	AGA	AGA	CAG		
	CAG	ACT	ACT	GGT	GAC	ATG	TGC	GGT	GGT	GAC	GGT	GGG	TCT	TCT	GTC		
271	TGG	ATG	GAC	CCT	CTG	GTA	AAC	TGT	GGC	GTG	ATG	GCC	GTG	GTG	CTC		
	ACC	TAC	TAC	CTG	GGA	GAC	CAT	TTC	ACA	CCG	CAC	TAC	CGG	CAC	CAC	GAG	
316	AGC	AGA	ATA	TCA	TTC	CCG	CCG	AAT	TCC	CCA	GCC	GCA	GCT	AGC	TAA		
	TCG	TCT	TAT	AGT	AAG	GGC	GCC	TTC	AGG	GGT	CGG	CGT	CGA	TCG	ATT		

Title: METHOD FOR CONTROLLING  
GENE EXPRESSION IN A CELL

Inventor: Jepson et al.  
Atty Docket: 1392/4/3/2

Fig.2 i.

361 CCT GCA GAC ACA ACC CCT ACC TTC CAT GCC GTT ACC AAT GCC  
GGA CGT CGT CTG TGT TGG GGA TGG AAG GTA CGG CAA TGG TTA CGG  
406 ACC GAC AAC CAA ATC AGA AAA CGA GTC AAT GTC ATC AGG TCG  
TGG CTG TTG TGG GTT TAG TCT TTT GCT CAG TTA CAG TAG TCC AGC  
451 TGA GGA ACT GTC TCC AGC TTC GAG TGT AAA CGG CTG CAG CAC AGA  
ACT CCT TGA CAG AGG TCG AAG CTC ACA TTT GCC GAC GTC GTG TCT  
496 TGG CGA GGC GAG GCG GCA GAA GAA AGG CCC AGC GCC GAG GCA GCA  
ACC GCT CCG CTC CGC CGT CTT ACA GAC GTC TCC GGG TCG CGG CTC CGT CGT  
541 AGA AGA GCT ATG TCT TGT CTG CGG CGA CAG AGC CTC CGG ATA TCA  
TCT TCG CGA TAC AGA ACA GAC GTC TCG GAG GCC TAT AGT  
586 CTA CAA CGC GCT CAC ATG TGA AGG GTG TAA AGG TTT CTT CAG GCG  
GAT GTT GCG CGA GTG TAC ACT TCC CAC ATT TCC AAA GAA GTC CGC  
631 GAG TGT AAC CAA AAA TGC AGT GTA CAT ATG CAA ATT CGG CCA TGC  
CTC ACA TTG GTT TTT ACG TCA CAT GTA TAC GTT TAA GCC GGT ACG  
676 TTG CGA AAT GGA TAT CTA TAT GCG GAG AAA ATG TCA GGA GTG TCG  
AAC GCT TTA CCT ATA GAT ATA CGC CTC TTT TAC AGT CCT CAC AGC  
721 GTT GAA GAA ATG TCT TGC GGT GGG CAT GAG GCC CGA GTG CGT GGT  
CAA CTT CCT TAC AGA ACG CCA CCC GTA CTC CGG GCT CAC GCA CCA  
766 GCC GGA GAA CCA GTG TGC AAT GAA ACG GAA AGA GAA AAA GGC GCA  
CGG CCT CTT GGT CAC ACG TTA CTT TGC CTT TCT TGT TTT CCG CGT

Fig. 2 ii.

811 GAG GGA AAA AGA CAA ATT GCC CGT CAG TAC GAC GAC AGT AGA CGA  
CTC CCT TTT TCT GTT TAA CGG GCA GTC ATG CTG CTG TCA TCT GCT  
856 TCA CAT GCC TCC CAT GCA ATG TGA CCC TCC GCC CCC AGA GGC  
AGT GTA CGG AGG GTA CGT TAC ACT GGG AGG CGG TCT CCG  
901 CGC TAG AAT TCT GGA ATG TGT GCA CGA CGT GGT GCC ACG ATT  
GCG ATC TTA AGA CCT TAC ACA CGT GCT CCA CGG TGC TAA  
946 CCT GAA TGA GAA GCT AAT GGA ACA GAA CAG ATT GAA GAA CGT GCC  
GGA CTT ACT CTT CGA TTA CCT TGT CTT GTC TAA CTT CTT GCA CGG  
991 CCC CCT CAC TGC CAA TCA GAA GTC GTT GAT CGC AAG GCT CGT GTG  
GGG GGA GTG ACG GTT AGT CTT CAG CAA CTA GCG TTC CGA GCA CAC  
1036 GTA CCA GGA AGG CTA TGA ACA ACC TTC CGA GGA AGA CCT GAA GAG  
CAT GGT CCT TCC GAT ACT TGT TGG AAG GCT CCT TCT GGA CTT CTC  
1081 GGT TAC ACA GTC GGA CGA GGA CGA CGA AGA CTC GGA TAT GCC GTT  
CCA ATG TGT CAG CCT GCT CCT GCT GCT TCT GAG CCT ATA CGG CAA  
1126 CCG TCA GAT TAC CGA GAT GAC GAT TCT CAC AGT GCA GCT CAT CGT  
GGC AGT CTA ATG GCT CTA CTG CTA AGA GTG TCA CGT CGA GTA GCA  
1171 AGA ATT CGC TAA GGG CCT CCC GGG CTT CGC CAA GAT CTC GCA GTC  
TCT TAA GCG ATT CCC GGA GGG CCC GAA GCG GTT CTA GAG CGT CAG  
1216 GGA CCA GAT CAC GTT ATT AAA GGC GTG CTC AAG TGA GGT GAT GAT  
CCT GGT CTA GTG CAA TAA TTT CCG CAC GAG TTC ACT CCA CTA CTA  
1261 GCT CCG AGT GGC TCG GCG GTC TGA CGC GGC CAC CGA CAG CGT ACT  
CGA GGC TCA CGG AGC CGC CAT ACT GCG CCG GTG GCT GTC CGA TGA

Fig.2 iii.

1306	GTT	CGC	GAA	CAA	CCA	GGC	GTA	CAC	TCG	CGA	CAA	CTA	CCG	CAA	GGC
	CAA	GGG	CTT	GTT	GGT	CCG	CAT	GTG	AGC	GCT	GTT	GAT	GGC	GTT	CCG
1351	AGG	CAT	GGC	GTA	CGT	CAT	CGA	GGA	CCT	GCT	GCA	CTT	CTG	TCG	GTG
	TCC	GTA	CGG	CAT	GCA	GTA	GCT	CCT	GGG	CGA	CGT	GAA	GAC	AGC	CAC
1396	CAT	GTA	CTC	CAT	GAT	GAT	GGG	TAA	CGT	GCA	TTA	TGC	GCT	GCT	TAC
	GTA	CAT	GAG	GTA	CTA	CTA	CCT	ATT	GCA	CGT	AAT	ACG	CGA	CGA	ATG
1441	AGC	CAT	TGT	CAT	CTT	CTC	AGA	CCG	CGG	GCT	TGA	GCA	ACC	CCT	
	TCG	GTA	ACA	GTA	GAA	GAG	TCT	GGC	CGG	GCC	CGA	ACT	CGT	TGG	GGA
1486	GTT	GGT	GGA	GGA	CAT	CCA	GAG	ATA	TTA	CCT	GAA	CAC	GCT	ACG	GCT
	CAA	CCA	CCT	CCT	GTA	GGT	CTC	TAT	AAT	GGA	CTT	GTG	CGA	TGC	CCA
1531	GTA	CAT	CCT	GAA	CCA	GAA	CAG	CGC	GTC	GCC	CGG	CGG	CGT	CAT	
	CAT	GTA	GGA	CTT	GGT	CTT	GTC	GGC	CAG	CGG	GCC	GCC	GCG	GCA	GTA
1576	CTT	CGG	CGA	GAT	CCT	GGG	CAT	ACT	GAC	GGA	GAT	CGG	CAC	GCT	GGG
	GAA	GCC	GCT	CTA	GGA	CCC	GTA	TGA	CTG	CCT	CTA	GGC	GTG	CGA	CCC
1621	CAT	GCA	GAA	CTC	CAA	CAT	GTG	CAT	CTC	CCT	CAA	GCT	GAA	GAA	CAG
	GTA	CGT	CTT	GAG	GTT	GTA	CAC	GTA	GAG	GGA	GTT	CGA	CTT	CTT	GTC
1666	GAA	GCT	GCC	GCC	GTT	CCT	CGA	GGA	GAT	CTG	GGA	CGT	GGC	GGG	CGT
	CTT	CGA	CGG	CGG	CAA	GGA	GCT	CCT	CTA	GAC	CCT	GCA	CCG	CCT	GCA
1711	GGC	GAC	GAC	GGC	GAC	GCC	GGT	GGC	GGG	GGA	GGC	GCC	GCC	TCT	
	CCG	CTG	CTG	CCG	CTG	CGG	CCA	CCG	CCG	CTT	CCG	CCG	CCG	CGG	AGA

Fig. 2 iv.

1756	AGC	CCC	CGC	CCC	GCC	CGC	CGC	GCC	CGC	CAC	CGC	CGT	CTA	GCG	CGC
TCG	GGG	GAT	GCA	GAT	CGC	GCG	GCG								
1801	CTC	AGG	AGA	GAA	CGC	TCA	TAG	ACT	GGC	TAG	TTT	TAG	TGA	AGT	GCA
GAG	TCC	TCT	CTT	GGG	AGT	ATC	TGA	CCG	ATC	AAA	ATC	ACT	TCA	CGT	
1846	CGG	ACA	CTG	ACG	TCG	ACG	TGA	TCA	ACC	TAT	TAA	TAA	GGA	CTG	CGA
GCC	TGT	GAC	TGC	AGC	TGC	ACT	AGT	TGG	ATA	AAT	ATT	CCT	GAC	GCT	
1891	ATT	TTA	CCA	CTT	AAG	AGG	GCA	CAC	CCG	TAC	CCG	ATT	TCG	TAC	GG
TAA	AAT	GGT	GAA	TTC	TCC	CGT	GTG	GGC	ATG	GGC	TAA	AGC	ATG	CC	

Total number of bases is: 1934.

**Fig.3.**  
The sequence shown below is that of pSK16.1

Sequence ID3

3	9	15	21	27	33	39	45
1 CGC TGG TAT AAC AAC GGA CCA TTC CAG ACG CTG CGA ATG CTC GAG	GCG ACC ATA TTG TTG CCT GGT AAG GTC TGC GAC GCT TAC GAG CTC						
46 GAG AGC TCG TCT GAG GTG ACG TCG TCT TCA GCA CTG GGC CTG CCG	CTC TCG AGC AGA CTC CAC TGC AGC AGA AGT CGT GAC CCG GAC GGC						
91 CCG GCT ATG GTG ATG TCC CCG GAA TCG CTC GCG TCG CCC GAG ATC	GGC CGA TAC CAC TAC AGG GGC CTT AGC GAG CGC AGC GGG CTC TAG						
136 GGC GGC CTG GAG CTG TGG GGC TAC GAC GAT GGC ATC ACT TAC AGC	CCG CCG GAC CTC GAC ACC CCG ATG CTG CTA CCG TAG TGA ATG TCG						
181 ATG GCA CAG TCG CTG GGC ACC TGC ACC ATG GAG CAG CAG CCC	TAC CGT GTC AGC GAC CCG TGG ACG TGG TAC CTC GTC GTC GTC GGG						

**Fig.3 i.**

226	CAG	CCG	CAG	CAG	CCG	CAG	CAG	ACA	CAA	CCC	CTA	CCT	TCC	ATG
	GTC	GGC	GTC	GTC	GGC	GTC	GTC	TGT	TGT	GGG	GAT	GGA	AGG	TAC
271	CCG	TTA	CCA	ATG	CCA	CCG	ACA	ACA	CCC	AAA	TCA	GAA	AAC	GAG
	GGC	AAT	GGT	TAC	GGT	GGC	TGT	TGT	GGG	TTT	AGT	CTT	TTC	AGT
316	ATG	TCA	TCA	GGT	CGT	GAG	GAA	CTG	TCT	CCA	GCT	TCG	AGT	GTA
	TAC	AGT	AGT	CCA	GCA	CTC	CTT	GAC	AGA	GGT	CGA	AGC	TCA	CAT
361	GGC	TGC	AGC	ACA	GAT	GGC	GAG	GCG	AGG	CAG	AAG	AAA	GGC	CCA
	CCG	ACG	TCG	TGT	CTA	CCG	CTC	CGC	TCC	GCC	GTC	TTC	TTT	CCG
406	GCG	CCG	AGG	CAG	CAA	GAA	GAG	CTA	TGT	CTT	GTC	TGC	GAC	AGA
	CCG	GGC	TCC	GTC	GTT	CTT	CTC	GAT	ACA	GAA	CAG	ACG	CCG	CTG
451	GCC	TCC	GGA	TAT	CAC	TAC	AAC	GCG	CTC	ACA	TGT	GAA	GGG	TGT
	CGG	AGG	CCT	ATA	GTG	ATG	TTG	CGC	GAG	TGT	ACA	CTT	CCC	ACA
496	GGT	TTC	TTC	AGG	CGG	AGT	GTA	ACC	AAA	AAT	GCA	GTG	TAC	ATA

Fig.3 ii.

CCA AAG AAG TCC GCC TCA CAT TGG TTT TTA CGT CAC ATG TAT ACG  
541 AAA TTC GGC CAT GCT TGC GAA ATG GAT ATC TAT ATG CGG AGA AAA  
TTT AAG CCG GTA CGA ACG CTT TAC CTA TAG ATA TAC GCC TCT TTT  
586 TGT CAG GAG TGT CGG TTG AAG AAA TGT CTT GCG GTG GGC ATG AGG  
ACA GTC CTC ACA GCC AAC TTC TTT ACA GAA CGC CAC CCG TAC TCC  
631 CCC GAG TGC GTG CCG GAG AAC CAG TGT GCA ATG AAA CGG AAA  
GGG CTC ACG CAC CAC GGC CTC TTG GTC ACA CGT TAC TTT GCC TTT  
676 GAG AAA AAG GCG CAG AGG GAA AAA GAC AAA TTG CCC GTC ATG ACG  
CTC TTT TTC CGC GTC TCC CTT TTT CTG TTT AAC GGG CAG TCA TGC  
721 ACG ACA GTA GAC GAT CAC ATG CCT CCC ATC ATG CAA TGT GAC CCT  
TGC TGT CAT CTG CTA GTG TAC GGA GGG TAG TAC GTT ACA CTG GGA  
766 CCG CCC CCA GAG GCC GCT AGA ATT CTG GAA TGT GTG CAG CAC GAG  
GGC GGG GGT CTC CGG CGA TCT TAA GAC CTT ACA CAC GTC GTG CTC  
811 GTG GTG CCA CGA TTC CTG ATT GAG CTA ATG GAA CAG AAC AGA  
CAC CAC GGT GCT AAG GAC TTA CTC TTC GAT TAC CTT GTC TGT TCT  
856 TTG AAG AAC GTG CCC CCC ACT GCC AAT CAG AAG TCG TTG ATC  
AAC TTC TTG CAC GGG GGG GAG TGA CGG TTA GTC TTC AGC AAC TAG  
901 GCA AGG CTC GTG TGG TAC CAG GAA GGC TAT GAA CAA CCT TCC GAG  
CGT TCC GAG CAC ACC ATG GTC CTT CCG ATA CTT GGA AGG CTC  
946 GAA GAC CTG AAG AGG GTT ACA CAG TCG GAC GAG GAC GAA GAC  
CTT CTG GAC TTC TCC CAA TGT GTC AGC CTG CTC CTG CTT CTG CTC

Fig.3 iii.

991	TCG	GAT	ATG	CCG	TTC	CGT	CAG	ATT	ACC	GAG	ATG	ACG	ATT	CTC	ACA
AGC	CTA	TAC	GGC	AAG	GCA	GTC	TAA	TGG	CTC	TAC	TGC	TAA	GAG	TGT	
1036	GTG	CAG	CTC	ATC	GTA	GAA	TTC	GCT	AAG	GGC	CTC	CCG	GGC	TTC	GCC
CAC	GTC	GAG	TAG	CAT	CTT	AAG	CGA	TTC	CCG	GAG	GGC	CCG	AAG	CGG	
1081	AAG	ATC	TCG	CAG	TCG	GAC	CAG	ATC	ACG	TTA	TAA	AAG	GCG	TGC	TCA
TTC	TAG	AGC	GTC	AGC	CTG	GTC	TAG	TGC	AAT	TTA	CGC	ACG	AGT		
1126	AGT	GAG	Gtg	ATG	ATG	CTC	CGA	GTG	GCT	CGG	CGG	TAT	GAC	GCG	GCC
TCA	CTC	CAC	TAC	TAC	GAG	GCT	CAC	CGA	GCC	GCC	GCC	ATA	CTG	CGC	CGG
1171	ACC	GAC	AGC	GTA	CTG	TTC	GCG	AAC	AAC	CAG	GCG	TAC	ACT	CGC	GAC
TGG	CTG	TCG	CAT	GAC	AAG	CGC	TTG	TTG	GTC	CGC	ATG	TGA	GCG	CTG	
1216	AAC	TAC	CGC	AAG	GCA	GGC	ATG	GCG	TAC	GTC	ATC	GAG	GAC	CTG	CTG
TTG	ATG	GCG	TTC	CGT	CCG	TAC	CGC	ATG	CAG	TAG	CTC	CTG	GAC	GAC	
1261	CAC	TTC	TGT	CGG	TGC	ATG	TAC	TCC	ATG	ATG	ATG	GAT	AAC	GTG	CAT
GTG	AAG	ACA	GCC	ACG	TAC	ATG	AGG	TAC	TAC	TAC	TAC	CTA	TTG	CAC	GTA
1306	TAT	GCG	CTG	CTT	ACA	GCC	ATT	GTC	ATC	TTC	TCA	GAC	CGG	CCC	GGG
ATA	CGC	GAC	GAA	TGT	CGG	TAA	CAG	TAG	AAG	AGT	CTG	GCC	GGG	CCC	
1351	CTT	GAG	CAA	CCC	CTG	TTG	GTG	GAG	ATC	CAG	AGA	TAT	TAC	CTG	
GAA	CTC	GTT	GGG	GAC	AAC	CAC	CTC	CTG	TAG	GTC	TCT	ATA	ATG	GAC	
1396	AAC	ACG	CTA	CGG	GTG	TAC	ATC	CTG	AAC	CAG	AAC	AGC	GCG	TCG	CCC
TTG	TGC	GAT	GCC	CAC	ATG	TAG	GAC	TTC	GTC	TTC	TCT	GCG	AGC	GGG	
1441	CGC	GGC	GCC	GTC	ATC	TTC	GGC	GAG	ATC	CTG	GGC	ATA	CTG	ACG	GAG

**Fig.3 iv.**

GGC	CCG	CGG	CAG	TAG	AAG	CCG	CTC	TAG	GAC	CCG	TAT	GAC	GGC	CTC	
1486	ATC	CGC	ACG	CTG	GGC	ATG	CAG	AAC	TCC	AAC	ATG	TGC	ATC	TCC	CTC
TAG	GCG	TGC	GAC	CCG	TAC	GTC	GTC	TTG	AGG	TTG	TAC	ACG	TAG	AGG	GAG
1531	AAG	CTG	AAG	AAC	AGG	AAG	CTG	CCG	CCG	TTC	CTC	GAG	GAG	ATC	TGG
TTC	GAC	TTC	TTC	TTC	TTC	TTC	GAC	GAC	GGC	AAG	GAG	CTC	CTC	TAG	ACC
1576	GAC	GTG	GGC	GAC	GTG	GGC	ACG	ACG	GCG	ACG	CCG	GTG	GCG	GCG	GAG
CTG	CAC	CGC	CTG	CAC	CGC	TGC	TGC	TGC	CGC	TGC	GGC	CAC	CGC	CGC	CTC
1621	GCG	CCG	GCG	CCT	CTA	GCC	CCC	CCC	GCC	CCC	GCC	CGG	CGG	CCC	GCC
CGC	GGC	GGC	GGG	GGA	GAT	GGG									
1666	ACC	GTC	TAG	CGC	GCC	TCA	GGG	GAG	AAC	GCT	CAT	AGA	CTG	GCT	AGT
TGG	CAG	ATC	GGC	CGG	CGG	AGT	CCT	CTC	CTC	TTG	CGA	GTA	TCT	GAC	CGA
1711	TTT	AGT	GAA	GTG	CAC	GGA	CAC	TGA	CGT	CGA	CGT	GAT	CAA	CCT	ATT
AAA	TCA	CTT	CAC	GTG	CCT	GTG	ACT	GCA	GCT	GCA	GCT	GCA	CTA	GTT	GGA
1756	TAT	AAG	GAC	TGC	GAA	TTT	TAC	CAC	TTA	AGA	GGG	CAC	ACC	CGT	ACC
ATA	TTC	CTG	ACG	CTT	AAA	ATG	GTG	AAT	TCT	CCC	GTG	TGG	GCA	TGG	
1801	CGA	TTT	CGT	ACG	TAT	TCG	GTG	ACC	GAC	GAT	GCA	GAG	CGT	GTG	
GCT	AAA	GCA	TGC	ATA	AGC	CAC	TGG	CTG	CTG	CTA	CGT	CTC	GCA	CAC	
1846	TAA	TGT	GAA	TAT	ATG	TGT	TGT	TGA	ACG	ATT	TGG	AGA	ATA	TAT	ATT
ATT	ACA	CTT	ATA	TAC	ACA	ACA	ACA	ACT	TGC	TAA	ACC	TCT	TAT	ATA	TAA
1891	GGT	GTT	GCT	GTT	CGG	GGC	CGC	ACG	CCG	TGC	CCG	GTC	GGC	GGC	GAT
CCA	CAA	CGA	CAA	GCC	CGG	GGC	TGC	GGC	GGC	AGC	GGC	CAG	CCG	CCG	CTA

**Fig.3 V.**

1936 CGC GGC GCC CGC GGC TTC AGT TTT ATT TCG TTT ACT GAG TTG  
GGC CCG CGG GCG CCG AAG TCA AAA TAA AGC AAA TGC TGA CTC AAC

1981 GTC ACT CGG ATA CGA CTG TAT GAT AAG ACT TCG TTC GAT AAG TAC  
CAG TGA GCC TAT GCT GAC ATA CTA TTC TGA AGC AAG CTA TTC ATG

2026 ACC TAC TAA ATT ACA CAT ACG TAC GTA GCT TAC GAG AGT ATT TAG  
TGG ATG ATT TAA TGT GTA TGC ATG CAT CGA ATG CTC TCA ATA ATC

2071 AGA CAA AGA ATA TAA GAA GAA GAT GTT TCT ATT GGG TGA AAA GTT  
TCT GTT TCT TAT ATT CTT CTT CTA CAA AGA TAA CCC ACT ATT CAA

2116 GAT AGT TAT GTT TAT TTA CCA AAA TTA ACA ATA ATA CGT TGA TTA  
CTA TCA ATA CAA ATA AAT GGT TTT AAT TGT TAT TAT GCA ACT ATT

2161 ACC TTT CGA GTA TAA TAT TGT GAT GAG TCG TCC GCT GTC CAC GTC  
TGG AAA GCT CAT ATT ATA ACA CTA CTC AGC AGG CGA CAG GTG CAG

2206 GCC GTC ACA TGT TTG TTT CTG ATG CAC ACG TGA GGN GCG TTA TCG  
CGG CAG TGT ACA AAC AAA GAC TAC GTG ACT CCN CGC AAT AGC

2251 TGT TTC ATG GTT CCA TCG TCC TGT GCC CGC GAC CCT CGA CTA ATT  
ACA AAG TAC CAA GGT AGC AGG ACA CGG CTG GGA GCT GAT TTA

2296 GAG TAA TTT AAT TTA TTG CTG TGA TTA CAT ATT GTG TTG ATT  
CTC ATT AAA TTA AAT AAC GAC ACT ATT GAA TAA TTA CAC AAC TAA

2341 ATC TAC CAT AGG GTG ATA TAA GTG TGT CTT ATT ACA ATA CAA AGT  
TAG ATG GTA TCC CAC TAT ATT CAC ACA GAA TAA TGT TAT GTT TCA

2386 GTG TGT CGT CGA TAG CTT CCA CAC GAG CAA GCC TTT TGT TTA AGT

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**Fig.3 vi.** CAC ACA GCA GCT ATC GAA GGT GTG CTC GTT CGG AAA ACA AAT TCA

2431 GAT TTA CTG ACA TGG ACA CTC GAC CCG GAA CTT C  
CTA AAT GAC TGT ACC TGT GAG CTG GGC CTT GAA G

Total number of bases is: 2464.

Fig. 4. Sentence ID 4

ACTCGGCTCTCACCTGTGGATTGTACTAGA  
 GCTCGAACGAACTCCGATTCGTTGCAAGTCCGATAGCTGATAGGA  
 TTCCGGTTCTGTTAACGTTGGCTAGACGAGTGTGCATGTCCATGAGT  
 10 20 30 40 50 60  
 | | | | |  
 ACTCGGCTCTCACCTGTGGATTGTACTAGA  
 GCTCGAACGAACTCCGATTCGTTGCAAGTCCGATAGCTGATAGGA  
 TTCCGGTTCTGTTAACGTTGGCTAGACGAGTGTGCATGTCCATGAGT  
 70 80 90 100 110 120  
 | | | | |  
 ACTCGGCTCTCACCTGTGGATTGTACTAGA  
 GCTCGAACGAACTCCGATTCGTTGCAAGTCCGATAGCTGATAGGA  
 TTCCGGTTCTGTTAACGTTGGCTAGACGAGTGTGCATGTCCATGAGT  
 130 140 150 160 170 180  
 | | | | |  
 ACTCGGCTCTCACCTGTGGATTGTACTAGA  
 GCTCGAACGAACTCCGATTCGTTGCAAGTCCGATAGCTGATAGGA  
 TTCCGGTTCTGTTAACGTTGGCTAGACGAGTGTGCATGTCCATGAGT

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Fig.4 i.

190      200      210      220      230      240  
 |      |      |      |      |  
 AGTTAGTGGGAGAAAGTGAAGCTGGCTTCCTGGAGATGTCCCTGGGGTC  
 M S L G A  
 250      260      270      280      290      300  
 |      |      |      |  
 GTGGATAACCGAGGTGACACCGCTCGCCGACATGAGACGCCGCTGGTATAACAGGAC  
 R G Y R C D T L A D M R R W Y N N G  
 310      320      330      340      350      360  
 |      |      |  
 CATTCCAGACCGCTGGAAATGCTCGAGGAGAGCTCGTCACTGAGGTGACGGTCTTCAGCAC  
 P F Q T L R M L E E S S S E V T S S S A  
 370      380      390      400      410      420  
 |  
 TGGGCCTGCCGGCTATGGTGAATGCTCGGGAAATCGCTCGGGAGATCGGCG  
 L G L P P A M V M S P E S L A S P E I G

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Inventor: Jepson et al.  
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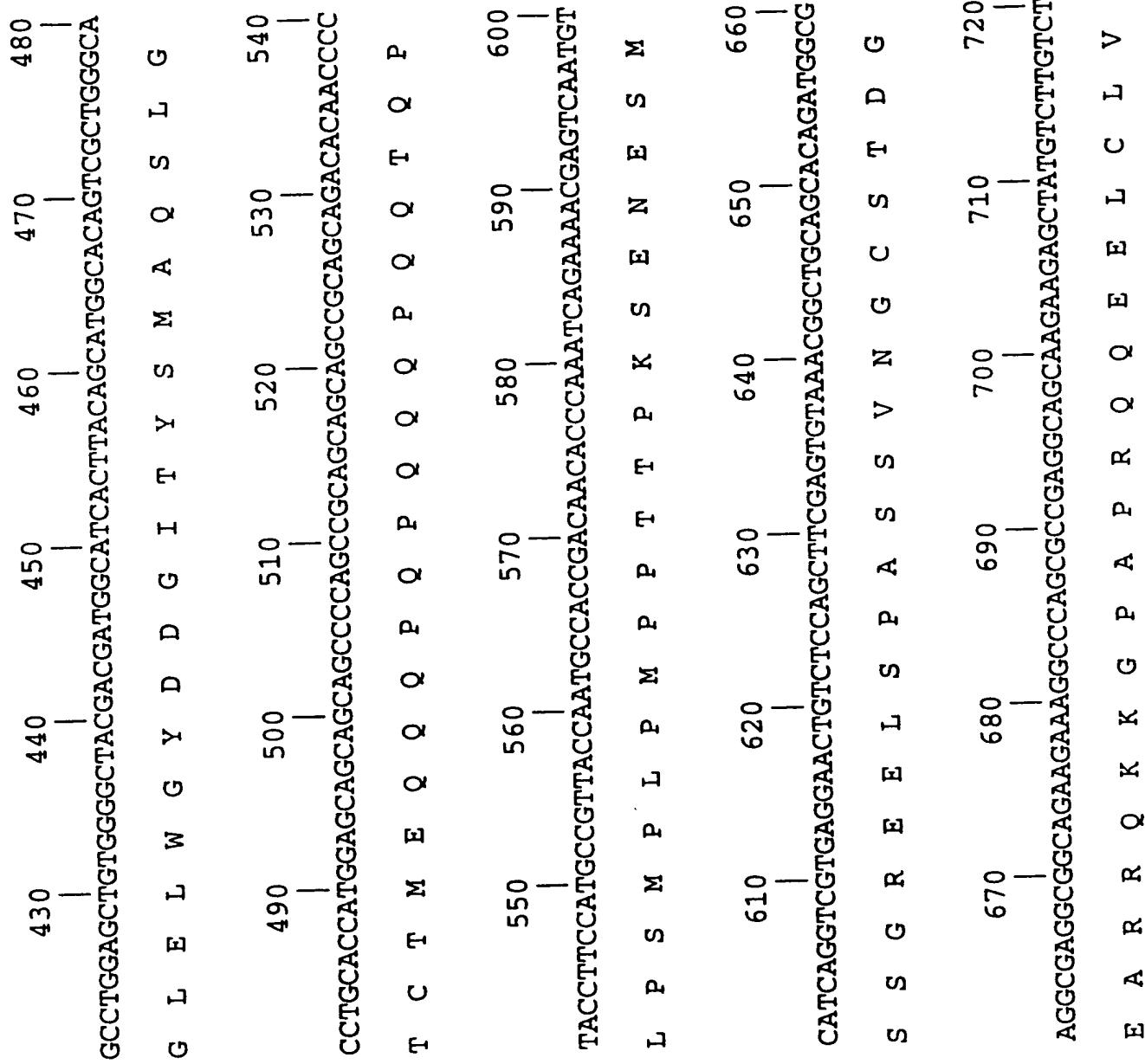


Fig.4 ii.

Title: METHOD FOR CONTROLLING  
GENE EXPRESSION IN A CELL  
Inventor: Jepson et al.  
Atty Docket: 1392/4/3/2

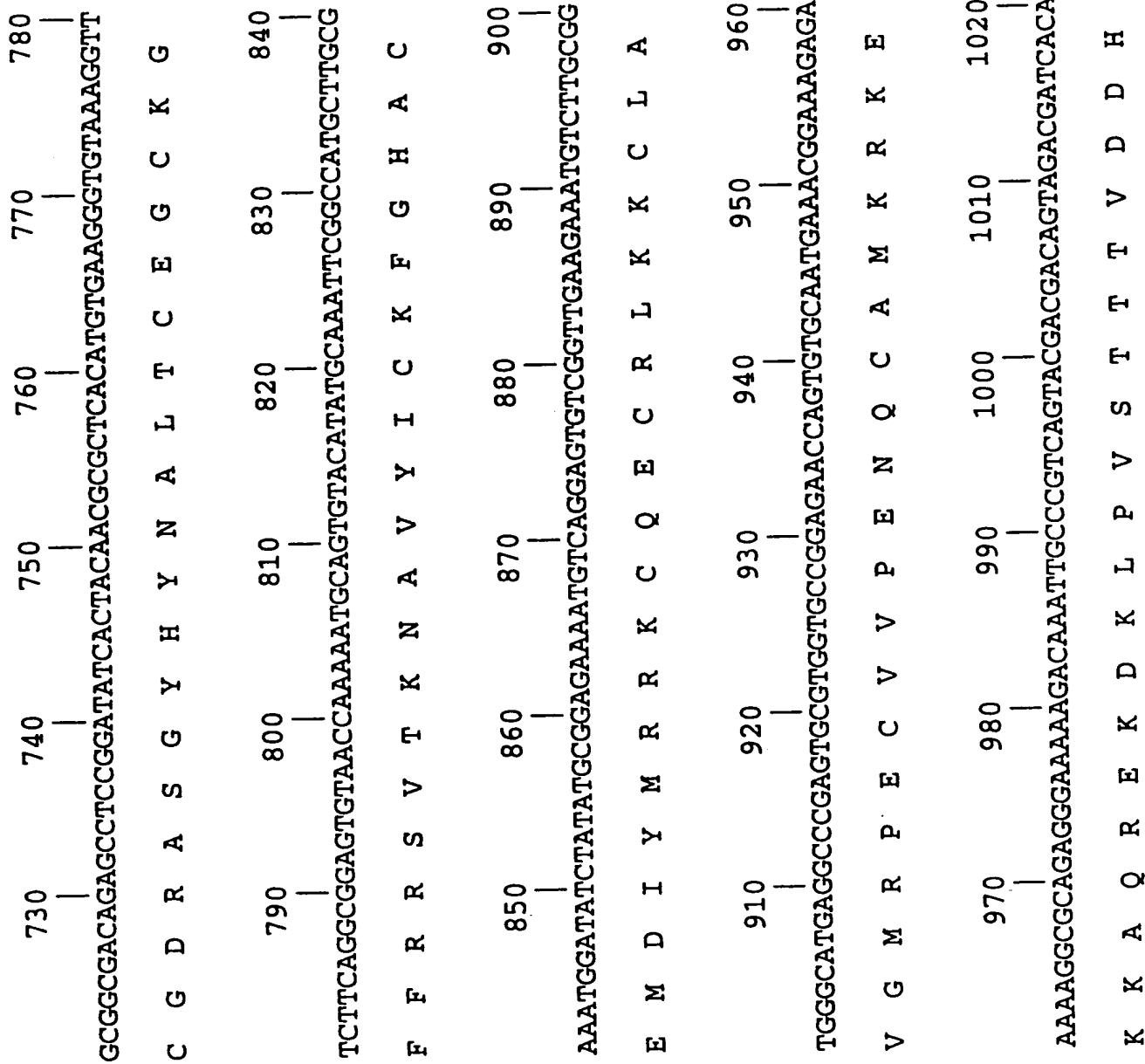


Fig.4 iv.

TGCCCTCCCATCATGCAATGTGACCCCTCGCCCCAGGGCCGCTAGAATTCTGGAAATGTG  
M P P I M Q C D P P P E A A R I L E C  
  
1090 1100 1110 1120 1130 1140  
TGCAGCAGGGTGGTGGCACCATTCCCTGAATGAGAACGCTAATGGAAACAGAACAGATTGA  
V Q H E V V P R F L N E K L M E Q N R L  
  
1150 1160 1170 1180 1190 1200  
AGAACCGTGCCTCCCCCTCACTGCCAATCAGAACGTTGATCGCAAGGCTCGTGTGGTACC  
K N V P P L T A N Q K S L I A R L V W Y  
  
1210 1220 1230 1240 1250 1260  
AGGAAGGCTATGAAACAAACCTTCGGAGGAAGACTGAAAGGGTTACACAGTCGGACGGG  
Q E G Y E Q P S E E D L K R V T Q S D E

Fig.4 v.

1270 |  
ACGACGGACTCGGATATGCCGTTCCGTCAAGATTACCGAGATGACGATTCTCACAGTGC  
D D E D S D M P F R Q I T E M T I L T V  
  
1330 |  
AGCTCATCGTAGAATT CGCTAAGGGCCTCCGGCTTCGCCAAGATCTCGCAGTCGGACC  
Q L I V E F A K G L P G F A K I S Q S D  
  
1390 |  
AGATCACGTTATTAAAGGGCGTGGCTCAAGTGAGGTGATGCTCCGAGTGGCTCGGGGT  
Q I T L L K A C S S E V M M L R V A R R  
  
1450 |  
ATGACGGGCCACCGACAGCGTACTGTTGGCAACCAACCAGGGTACACTCGCGACAACT  
Y D A A T D S V L F A N N Q A Y T R D N

Fig.4 vi.

1510      1520      1530      1540      1550      1560  
|      |      |      |      |  
ACCGCAAGGCATGGCGTACGTCACTGAGGACCTGCTGCACTTCTGTCGGTGCATGT  
  
Y R K A G M A Y V I E D L L H F C R C M  
  
1570      1580      1590      1600      1610      1620  
|      |      |      |      |  
ACTCCATGATGGATAACGTOGCCATTATGGCCTTGCTTAACAGCCATTGTCAATCTCTCAG  
  
Y S M M D N V H Y A L L T A I V I F S  
  
1630      1640      1650      1660      1670      1680  
|      |      |      |  
ACCGGCCGGCTTGAGCAACCCCTGTTGGAGGAGATCCAGAGATTACCTGAACA  
  
D R P G L E Q P L L V E E I Q R Y Y L N  
  
1690      1700      1710      1720      1730      1740  
|      |      |      |  
CGCTACGGGTGTACATCCTGAACCAGAACAGGGCGTGCCTGGCGGCATCTTCG  
  
T L R V Y I L N Q N S A S P R G A V I F

Fig.4 vii.

1750      1760      1770      1780      1790      1800  
|            |            |            |            |  
GCGAGATCCTGGGCATAACTGACGGAGATCCGCACGCTGGCATGCCAACATGGT

1810      1820      1830      1840      1850      1860  
|            |            |            |            |  
GCATCTCCCTCAAGCTGAAGAACAGGAAGCTGCCCGCTTCGAGGAGATCTGGGACG

C I S L K L R N R K L P P F L E E I W D

1870      1880      1890      1900      1910      1920  
|            |            |            |            |  
TGGCGGACCGTGGCGACGGCACGGCGACGGCGACGGCGGGAGGGCCCTAGCCC

V A D V A T T A T P V A A E A P A P L A

1930      1940      1950      1960      1970      1980  
|            |            |            |            |  
CCGGCCCCGCCGGCCACCGGTCTAGCGCCCTCAGGAGAAACGCTCATA

P A P P A R P P A T V -

1990      2000      2010      2020      2030      2040  
|            |            |            |            |  
GACTGGCTAGTTTAACTGAGCTGGCACGGACACTGACGTCGACTCAACCTATTATA

Fig. 4 viii.

2050      2060      2070      2080      2090      2100  
|      |      |      |      |  
AGGACTGCGAATTTCACCTTAAGAGGGCACACCCGTACCCGATTTCGTACGTATTTCGG

2110      2120      2130      2140      2150      2160  
|      |      |      |      |  
TGACCGACCGATGCCAGAGCCGTGCTGAATATGTGTTGAAACGGATTGGA

2170      2180      2190      2200      2210      2220  
|      |      |      |      |  
GAATATATTGGTGTGTTGCTGGGCCGCACGCCGTGGCGGATCCGCG

2230      2240      2250      2260      2270      2280  
|      |      |      |      |  
GGCCCCGGCTTCAGTTTATTTCGTTACGACTGAGTTGGTCACTCGGATAACGACTGT

2290      2300      2310      2320      2330      2340  
|      |      |      |      |  
ATGATAAGACTTCGTTCGATAAGTACACCTACTAAATTACACATAACGTTACG

2350      2360      2370      2380      2390      2400  
|      |      |      |      |  
AGAGTTTACGAGACAAAGAATAAGAAGATGTTCTATGGGTGAAAGTTGATA

Fig.4 ix.

2410      2420      2430      2440      2450      2460  
|      |      |      |      |  
GTTATGTTTACCAAAATTAAACAATAAACGTTGATTAACCTTTGGAGTATAATATT

2470      2480      2490      2500      2510      2520  
|      |      |      |      |  
GTGATGAGTCGGTCCGGCTGTCCACAGTCGCCCGTCACATGTTTGTTCTGATGCACACCGTGAG

2530      2540      2550      2560      2570      2580  
|      |      |      |      |  
GNGCGTTATCGTGTTCATGGTTCCATCGTCCCTGTGCCCGACCCCTCCGACTAAATGAGT

2590      2600      2610      2620      2630      2640  
|      |      |      |      |  
AATTAAATTGCTGTGATTACATTTAACATGTTGATTATCTACCATAGGGTGATAT

2650      2660      2670      2680      2690      2700  
|      |      |      |      |  
AAGTGTTGCTTATTACAATAAACGTTGTTGCTGGATAGCTTCACACGAGCAAGCCT

2710      2720      2730      2740  
|      |      |  
TTTGTGTTAAGTGATTACTGACATGGACACTCGACCCGGAAACTTC

**Fig. 5.**

Sequence I.D. 5

BmECR	MRVENVDNVS	10						
MSECR	-----							
HVECR	M-----	1						
CtECR	-----							
AaECR	-----							
DmECR	-----							
BmECR	FALNGRADEWCMSVETRLDSLVREREKSEVKAYVGGCPSVITDAGAYDALEDF	60						
MSECR	-----							
HVECR	-----		DTLAD					
CtECR	-----		-----					
AaECR	-----		-----					
DmECR	-----		-----					
BmECR	M-RRRWISNNNGGF-P-LRMILEESSEVTSSA-LGLPPAMVMSPESLASPEY	107						
MSECR	M-RRRWISNNNGCF-P-LRMFEESSEVTSSA-FGMPAAMVMSPESLASPEY	47						
HVECR	M-RRRWYNNNGGFQTLRMILEESSEVTSSA-LGLPPAMVMSPESLASPEI	64						
CtECR	M-K-----TENLIVTT-VKVEPLNYASQSF	23						
AaECR	MKRRWISNNNGFTAIRMLDDSSSEVTSSAAL---GMTMSPNSLGSPPNY	46						
DmECR	M-KRRWISNNNGF---MRLPEEESSEVTSSSNGLVLPSGVNMSPSSLDSDHY	47	*	*	*	*	*	*

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**Fig. 5 i.**

BmECR	GALELW-----SY-----	114	55
M <sub>s</sub> ECR	GGLELW-----SY-----		72
H <sub>v</sub> ECR	GGLELW-----GY-----		33
C <sub>t</sub> ECR	GDNNTI-----YGGAT-----		78
A <sub>a</sub> ECR	DELELW-SSYEDNAYNGHSV--LSNGNNN-----LGCGA-----		78
D <sub>m</sub> ECR	CDNDKWLCGNESGSEFGSNGHGLSQQQSVITLAMHGCSSSTLPAQTTIIP		97
.			
BmECR	-----DDGITY-----	121	121
M <sub>s</sub> ECR	-----DETMTN-----		61
H <sub>v</sub> ECR	-----DDGIT-----		77
C <sub>t</sub> ECR	-----KKORILESDETMINH-----		46
A <sub>a</sub> ECR	-----ANNLMMNGIVGNNNL---NGMMN-----		98
D <sub>m</sub> ECR	INGNANGNGGSTNGQYVPGATNLGALANGMLNGFNGMQQQIQNGHGLIN		147
.			
BmECR	-----QOPHPAPPPLPTMP-----	154	154
M <sub>s</sub> ECR	-----QQQQPSAQPLPSMP-----		94
H <sub>v</sub> ECR	-----QQQPQQTQPLPSMP-----		114
C <sub>t</sub> ECR	-----QQQPQQTQPLPSMP-----		86
A <sub>a</sub> ECR	-----GFSSPDVNTYEAYSPNSKL-----DDGN-----		134
D <sub>m</sub> ECR	-----NQTMNMLESNNMNHTIS-----LINGVNPNQTLIPPLPS-----		197
.			
BmECR	-----NTAQSLLGACNMQQQLQP-----		190
M <sub>s</sub> ECR	-----YPAQSLLGACNAPOQQQQQ-----		130
H <sub>v</sub> ECR	-----YSMAQSLGTCTMEQQQPQP-----		146
C <sub>t</sub> ECR	-----NQTMNMLESNNMNHTIS-----MASQAVQANANSIQHIVGN-----		98
A <sub>a</sub> ECR	-----STTPSTPTPLHLQQNLLGGAGGGGIGGMGILHHANGTPNGLIGVVGFFF		173
D <sub>m</sub> ECR	-----.		247
.			
BmECR	-----L.PMPPTTPKSENESMSSGREELSPASSINGCSADA--D-----		*
M <sub>s</sub> ECR	-----L.PMPPTTPKSENESMSSGREELSPASSINGCSTDG--E-----		*
H <sub>v</sub> ECR	-----L.PMPPTTPKSENESMSSGREELSPASSINGCSTDG--E-----		*
C <sub>t</sub> ECR	-----MSVHMGDG-----		*
A <sub>a</sub> ECR	-----IIQNTLMTPRSESVNISISSGREDLSPSSSLNGYT--DGSD-----		*
D <sub>m</sub> ECR	-----VGLGVGGGGVGGGLGMQHTPRSDSVNISISSGRDDLSPPSSSLNGYSANESCD-----*		*
.			

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Fig. 5 ill.

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Fig. 5

## Fig. 5 IV.

BmECR	GTQNSNMCISLKLKNRKLPPFLEEIWVDVAEVARR-----	593
MsECR	GTQNSNMCISLKLKNRKLPPFLEEIWVDVAEVSTT-----	535
HvECR	GMQNSNMCISLKLKKRKLPFFLEEIWVDVADVATT-----	552
CtECR	GNLNSEMCFSLKLRRNRKLPRFLEEIVMDVGDNNTATTNTENIVRERIN	534
AaECR	GNQNSEMCFSLKLKNRKLPRFLEEIWVDVQDIPPSMQAQMHSHTQSSS--	590
DmECR	GNQNAEMCFSLKLKNRKLPKFLEEIWVDVHAIPPSVQSHLQITQEEDERLE	674
	* * * . * * * . . * * * . * * * . * * * . .	
BmECR	-----	593
MsECR	-----	535
HvECR	-----	552
RN	-----	536
	-----	
CtECR	-----	632
AaECR	-----	724
DmECR	RAERMRAVGGAITAGIDCDASASTSAAAAQHQPQPQPSLTLQND	
	-----	
BmECR	-----HPTV-----LPPTNPVVL-----	606
MsECR	-----QP---TPGVAAQVTPIVVDNPAA-----	556
HvECR	-----ATPVAAEAPPLAPAPPAPATV-----	575
CtECR	-----	536
AaECR	-----HSQLQQ-----V	645
DmECR	SQHQTQPQLQPQLQQPQLQPOLOTLQPOIQPQQLPVSAVP	774
	-----	
BmECR	-----	606
MsECR	-----	556
HvECR	-----	575
CtECR	-----	536
AaECR	-----HANGSGGGSNNNSSSG-----	663
DmECR	PASVTAPGSSLAVSTSSEYMGSSAAIGPITPATTSSITAATASSTTSBV	824

Fig. 5 V.

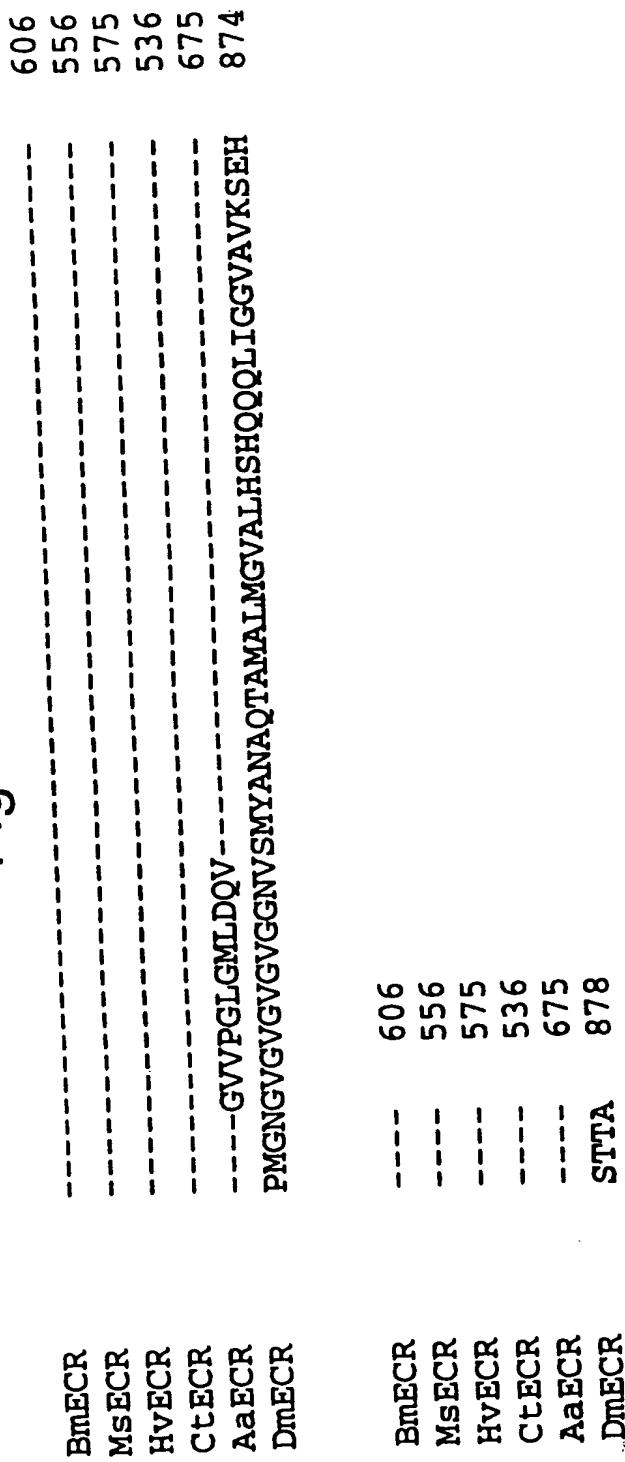
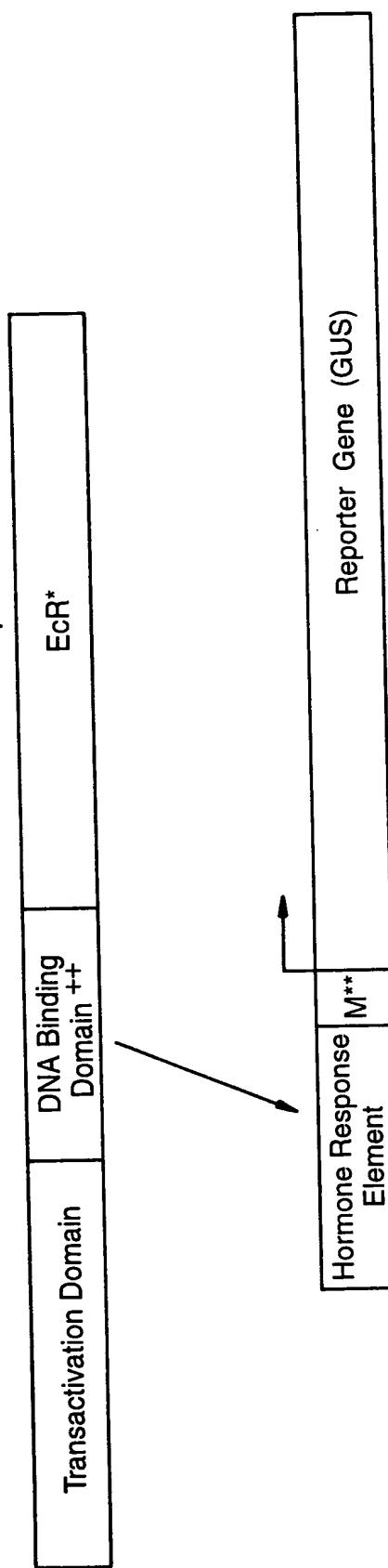


Fig. 6. Chemical



++ Glucocorticoid receptor DNA binding and transactivation domains  
\* Insect ecdysone ligand binding domain  
\*\* Minimal 35S CaMV promoter

Fig. 7.

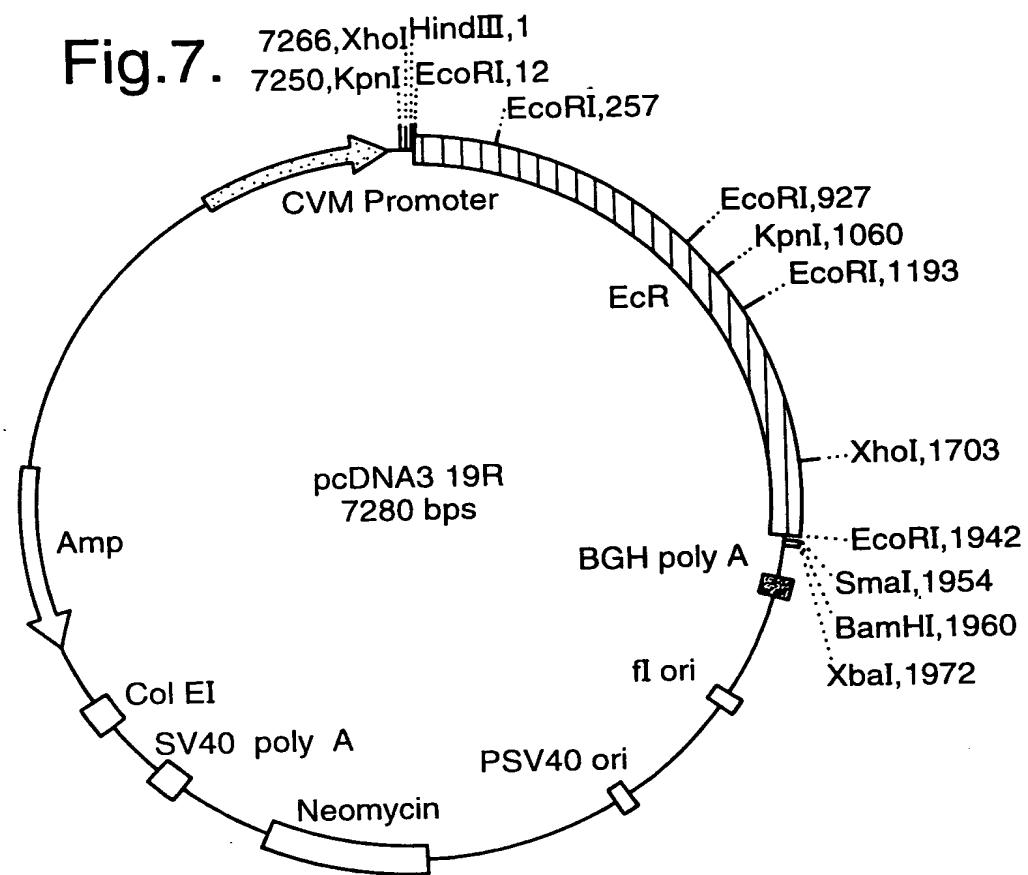


Fig. 8.

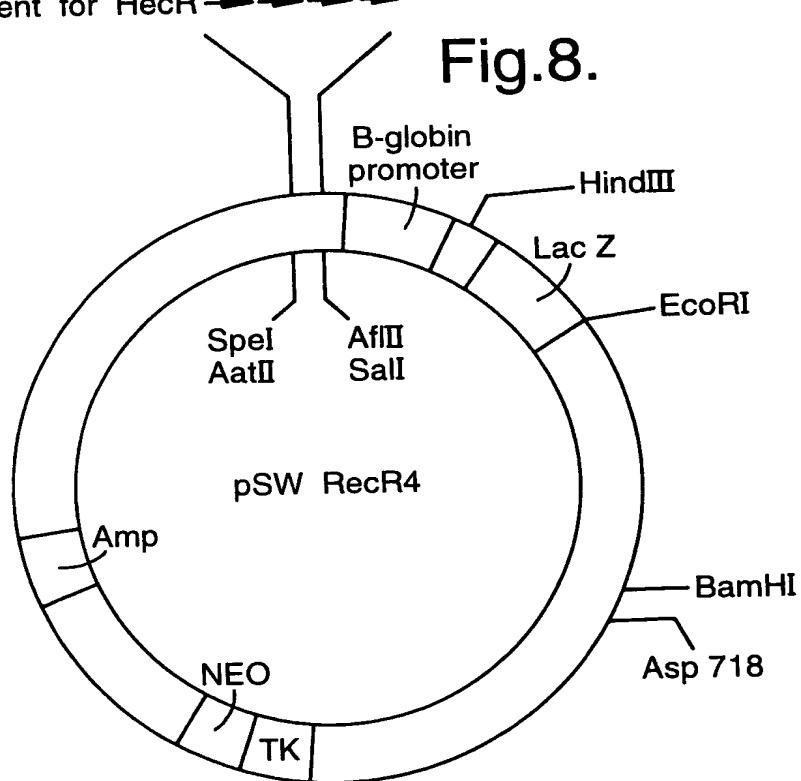


Fig.9.

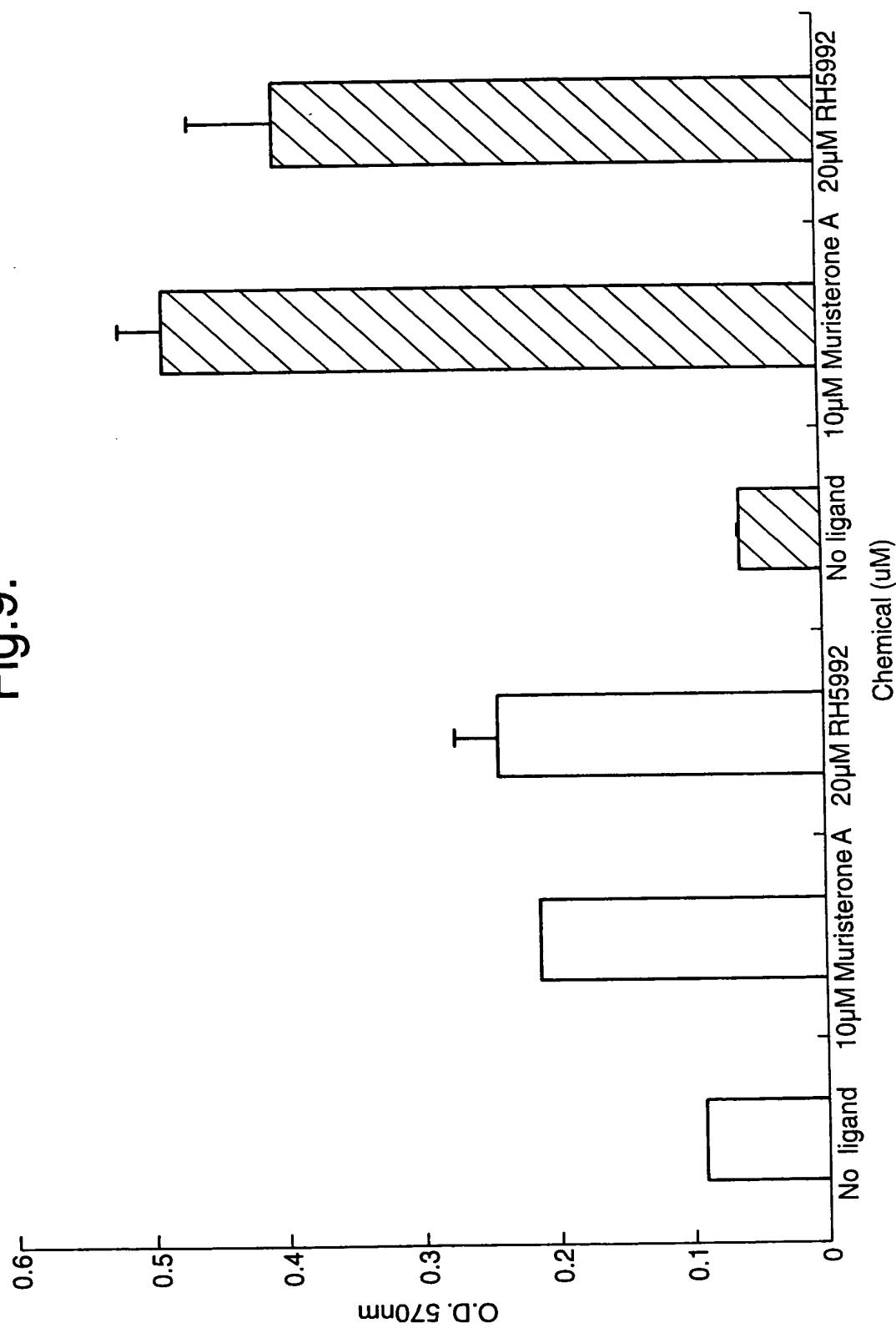


Fig.10.

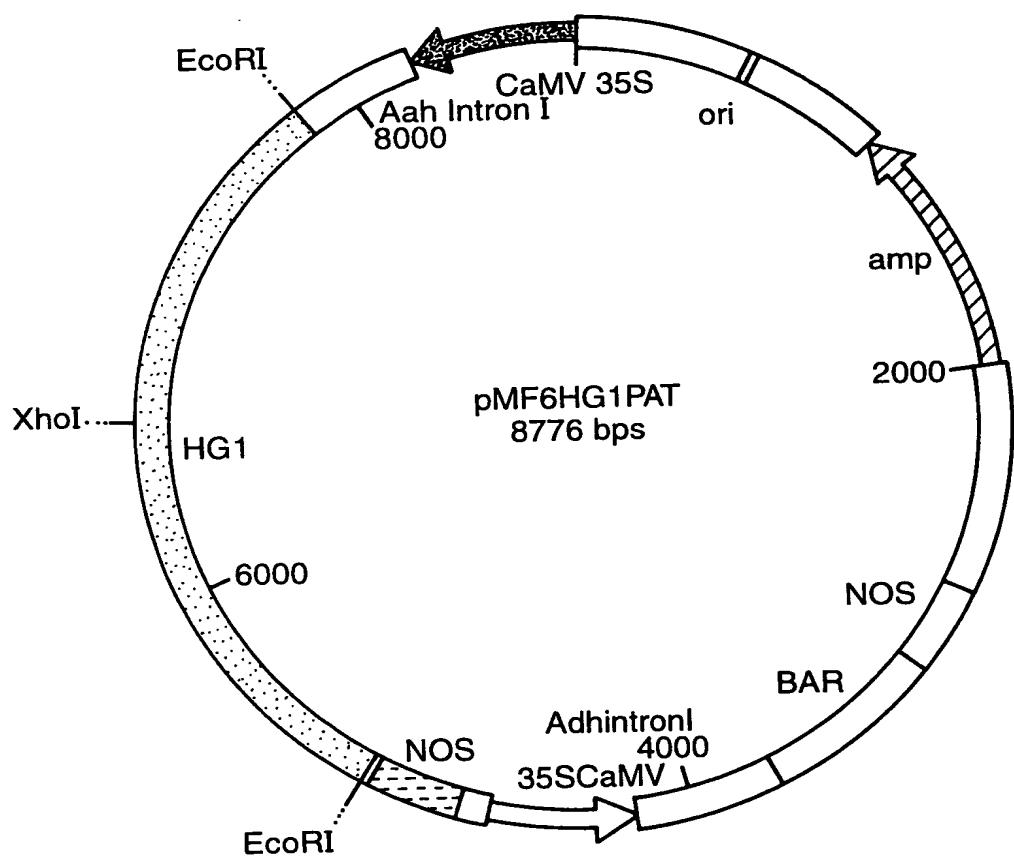


Fig.11.

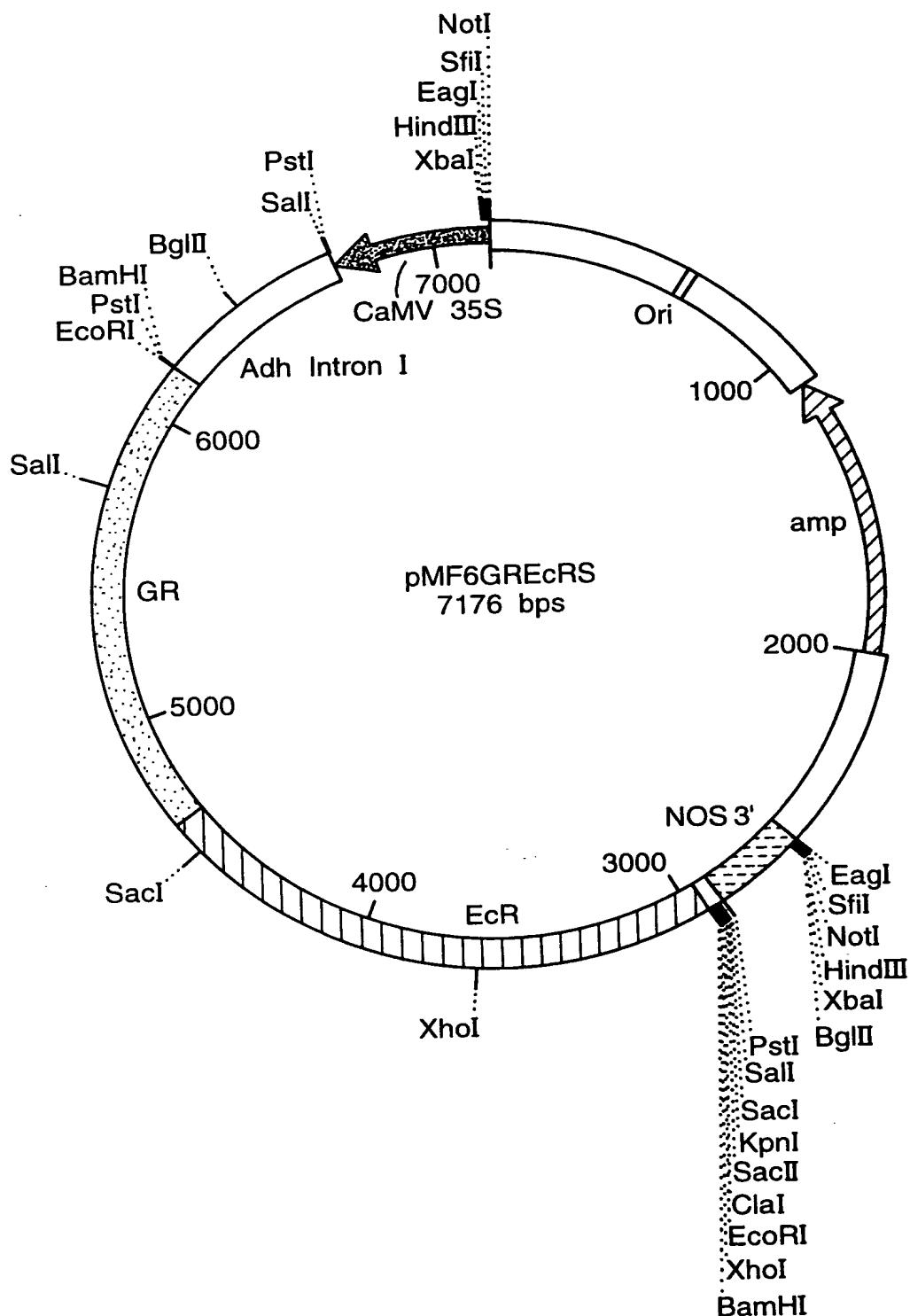


Fig. 12.

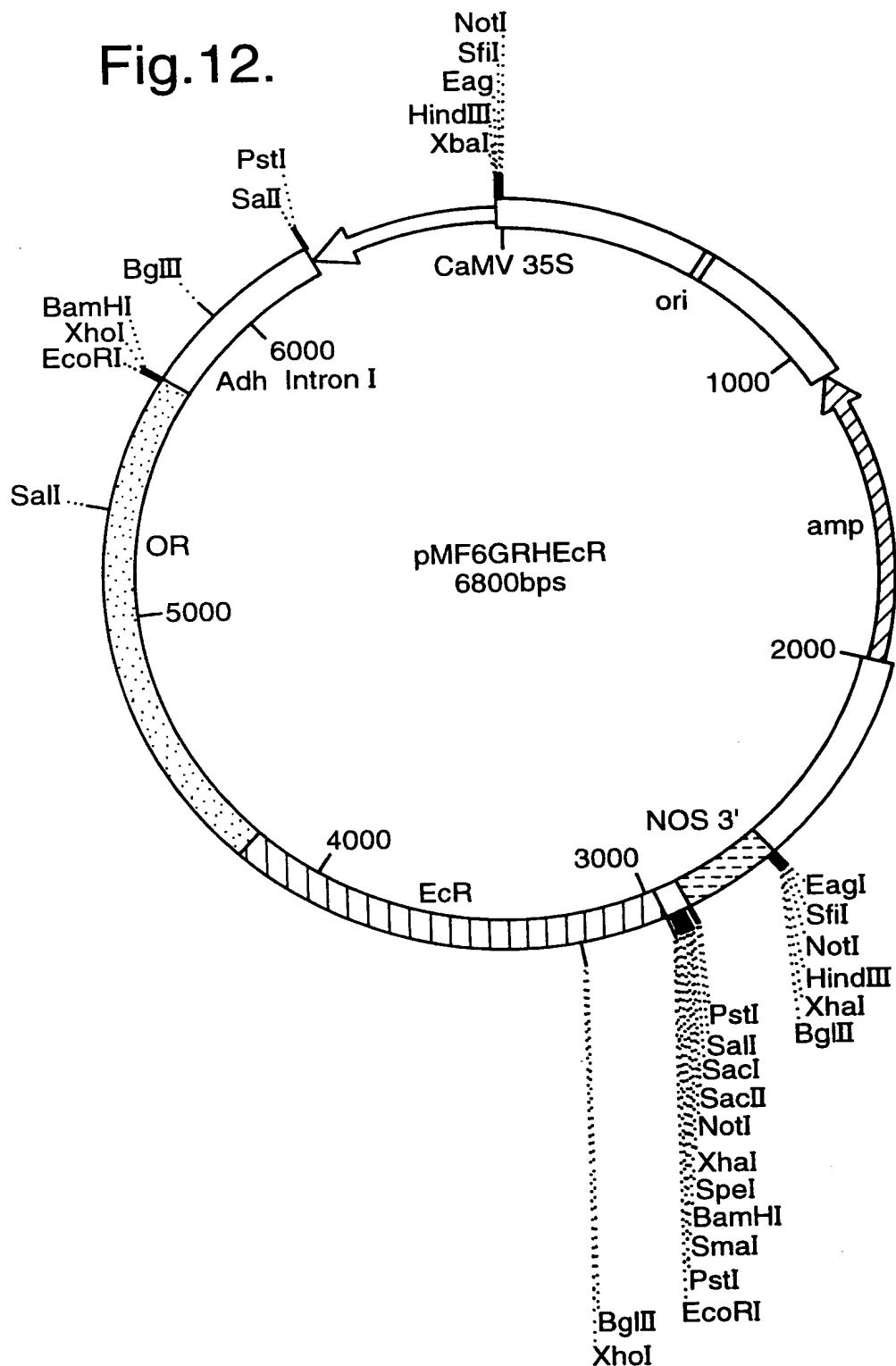


Fig.13.

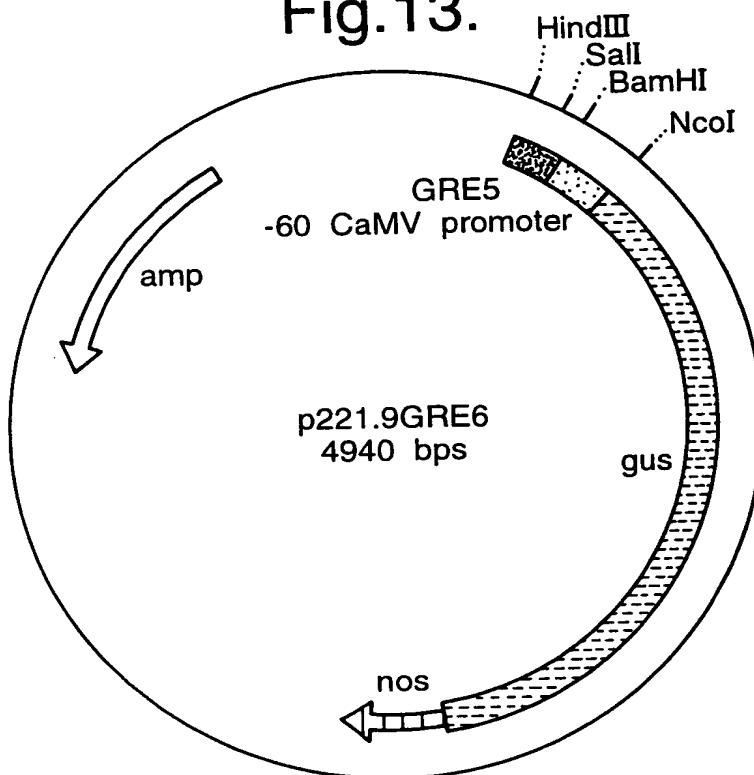


Fig.14.

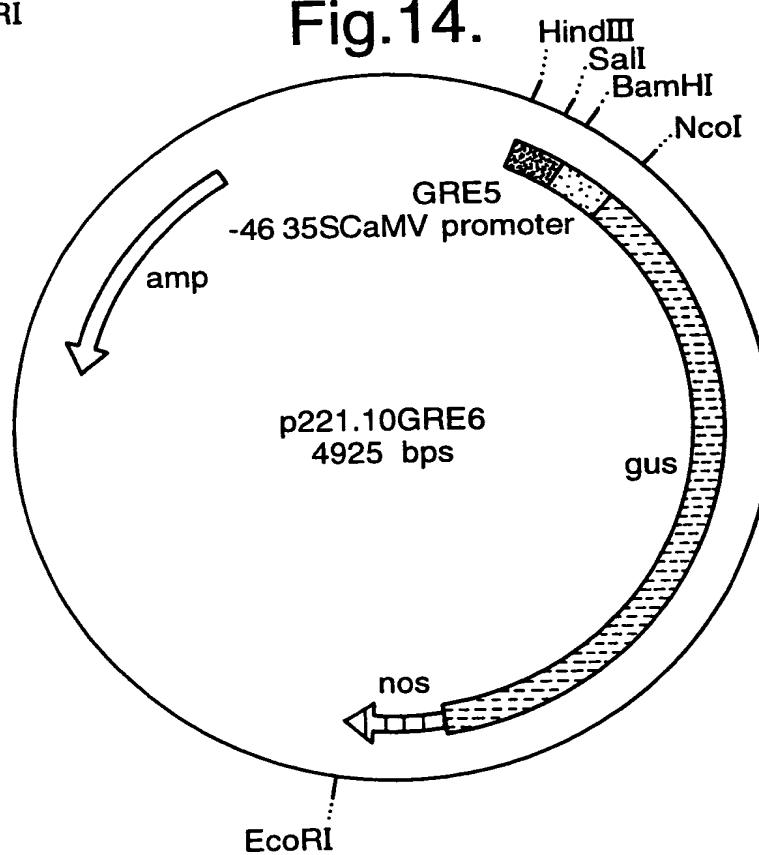


Fig.15.

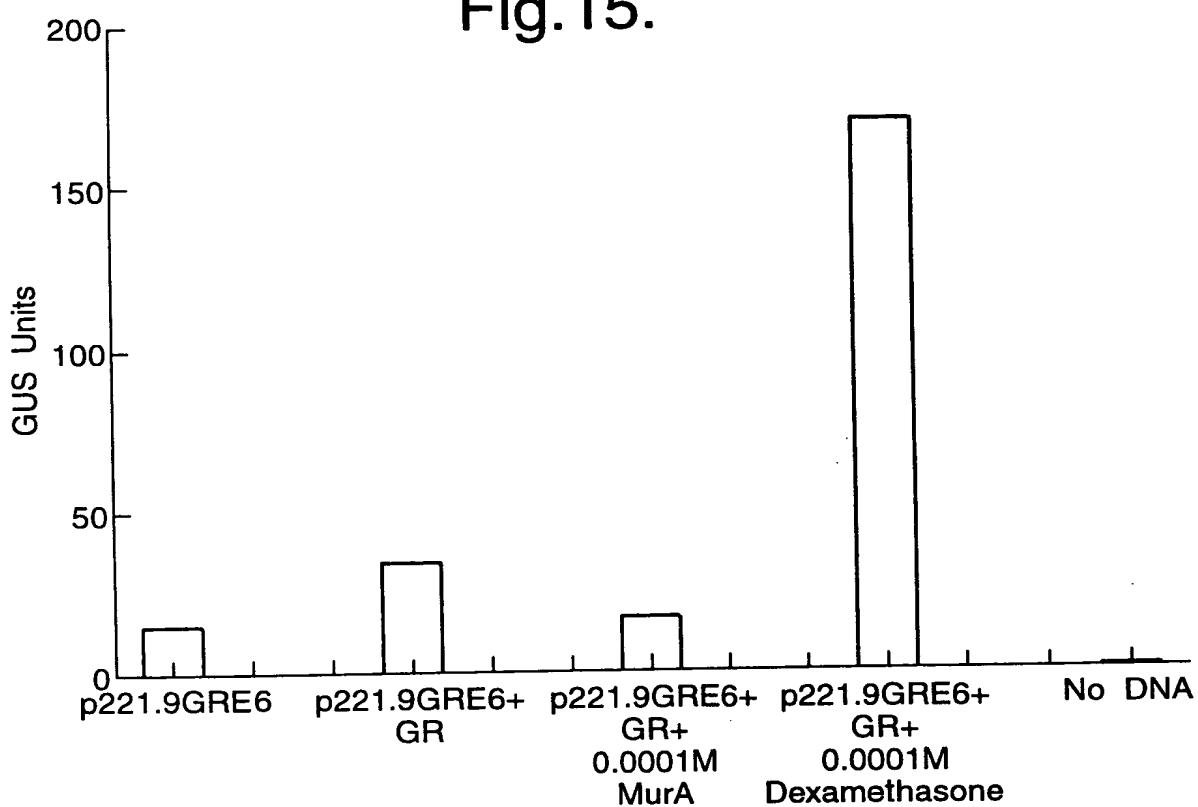


Fig.16.

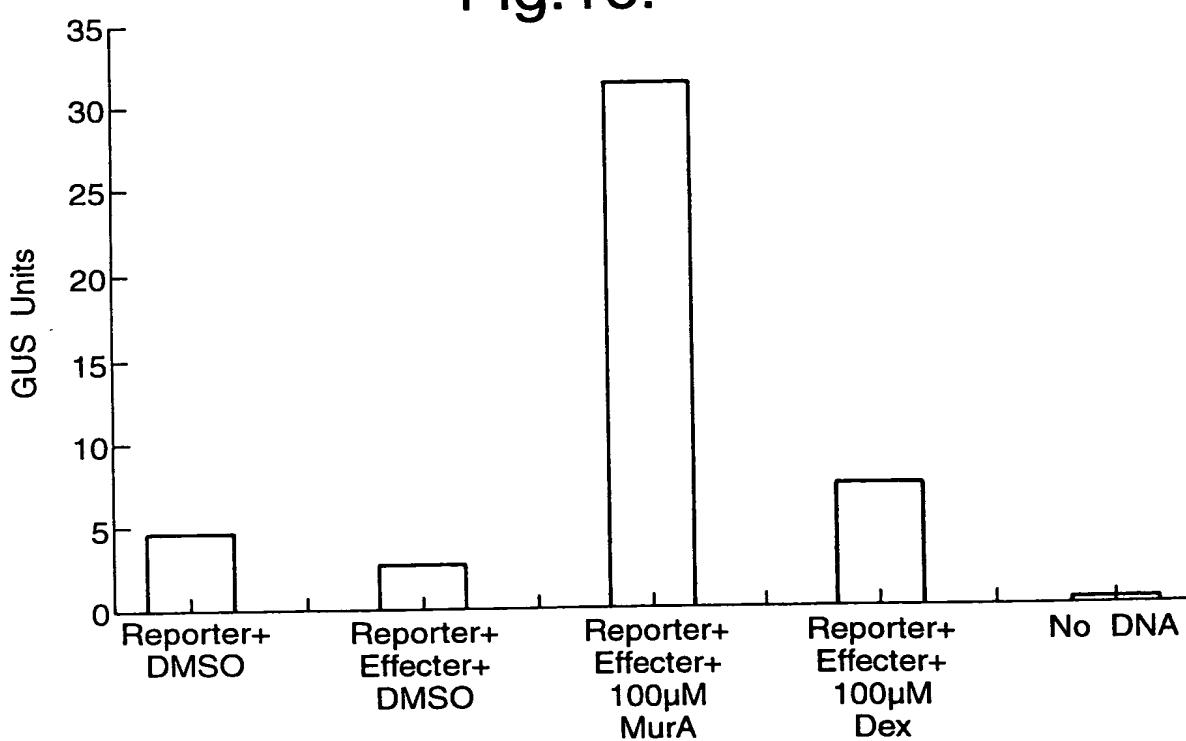


Fig.17.

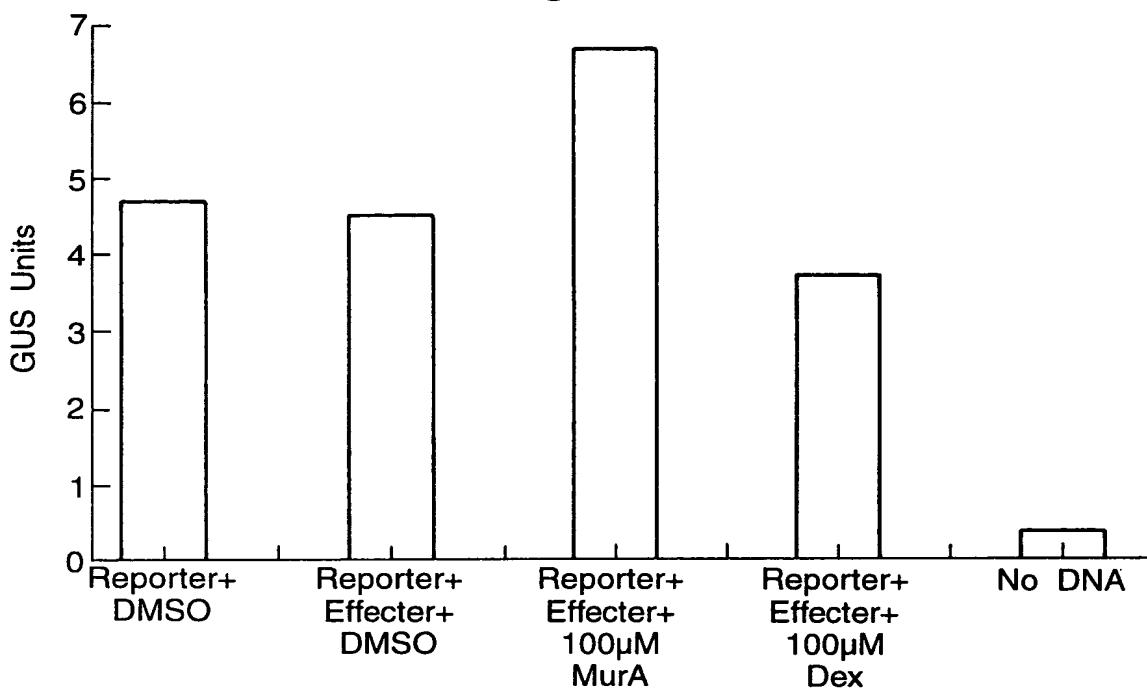


Fig.18.

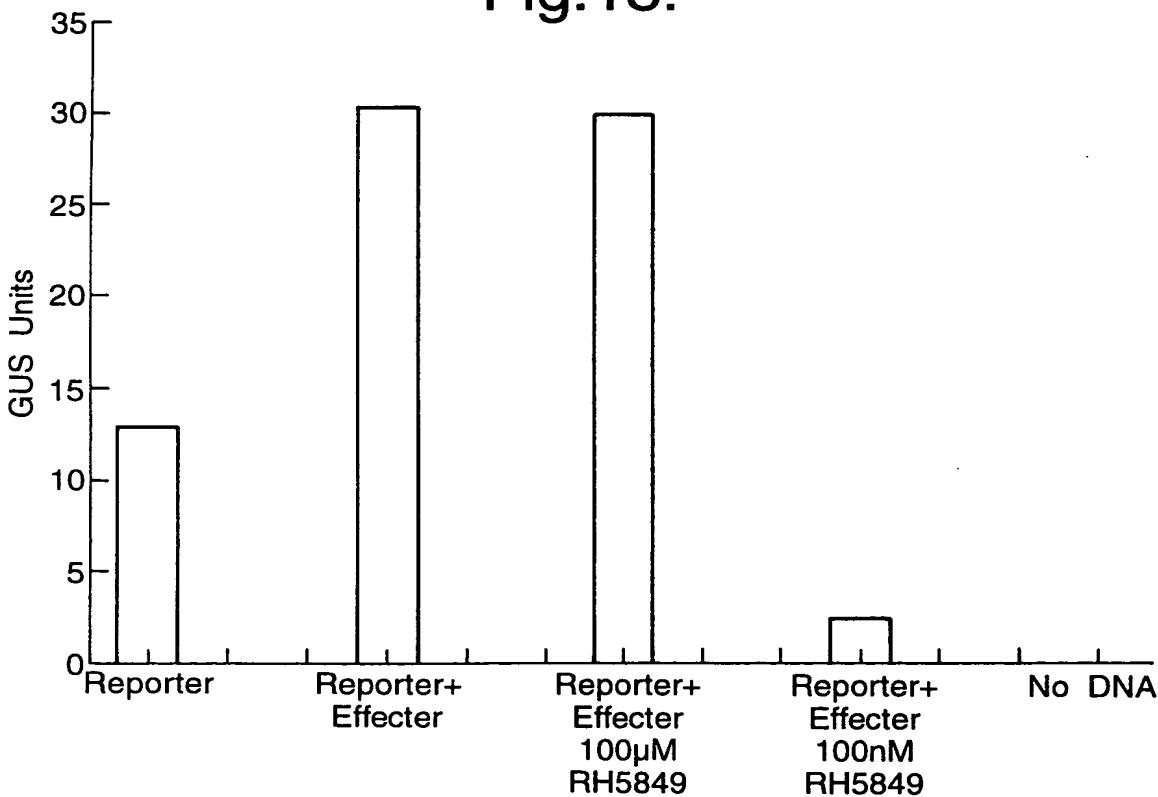


Fig.19.

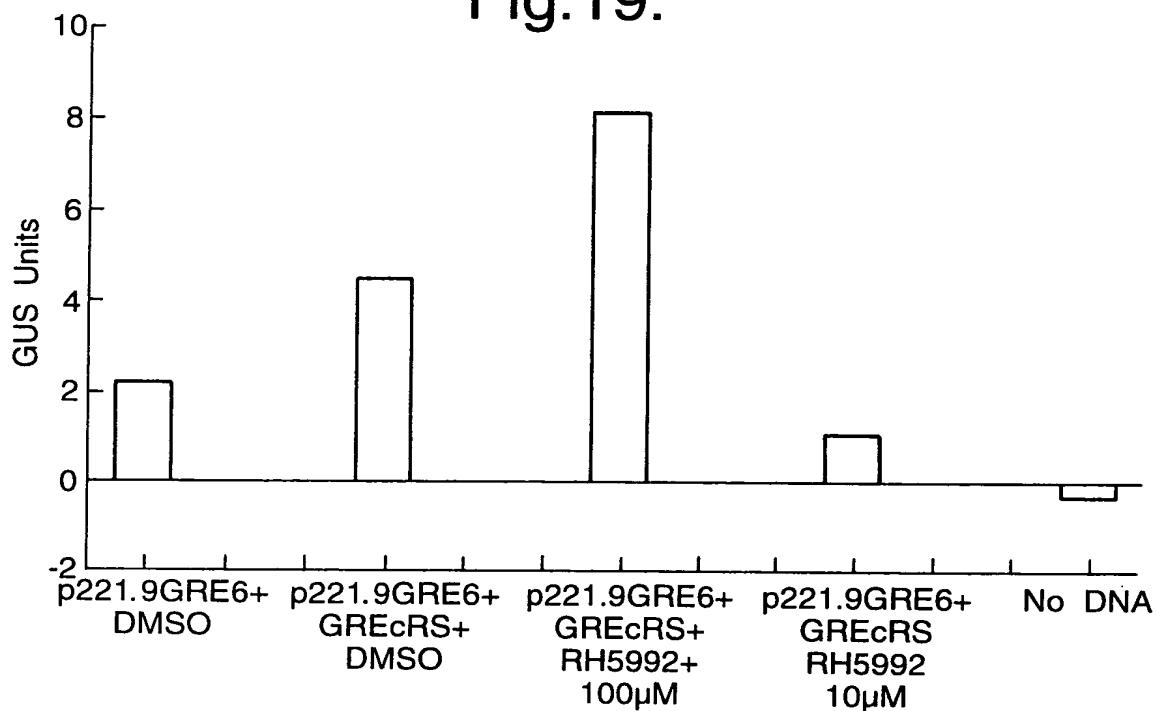
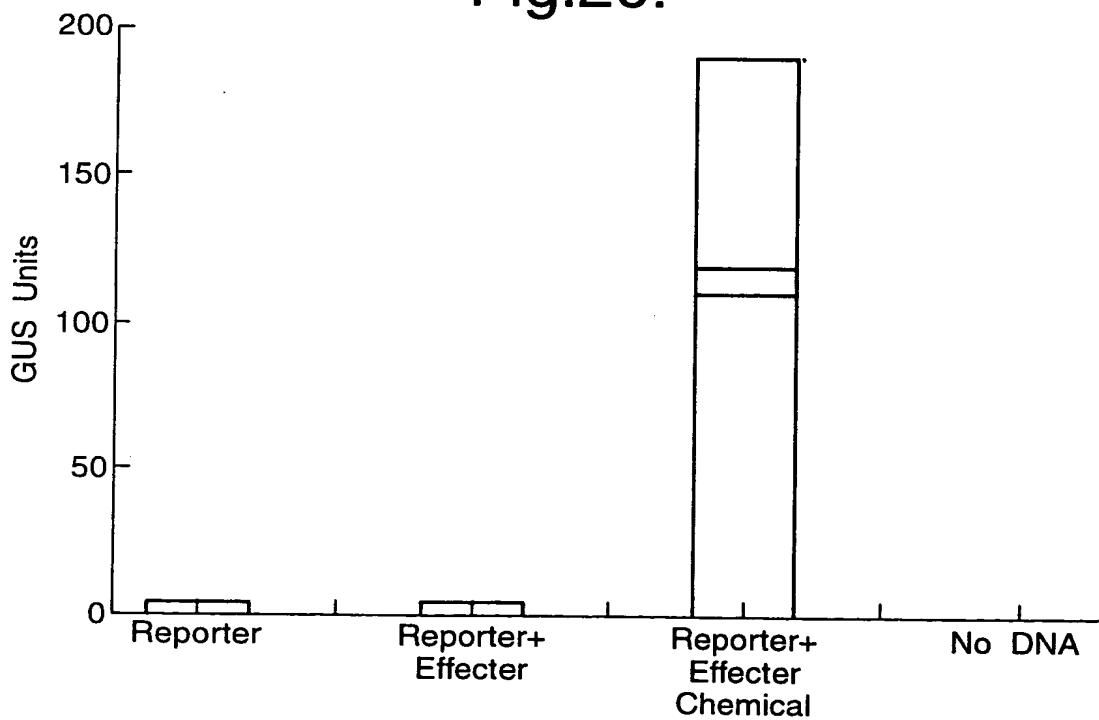


Fig.20.



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Fig.21.

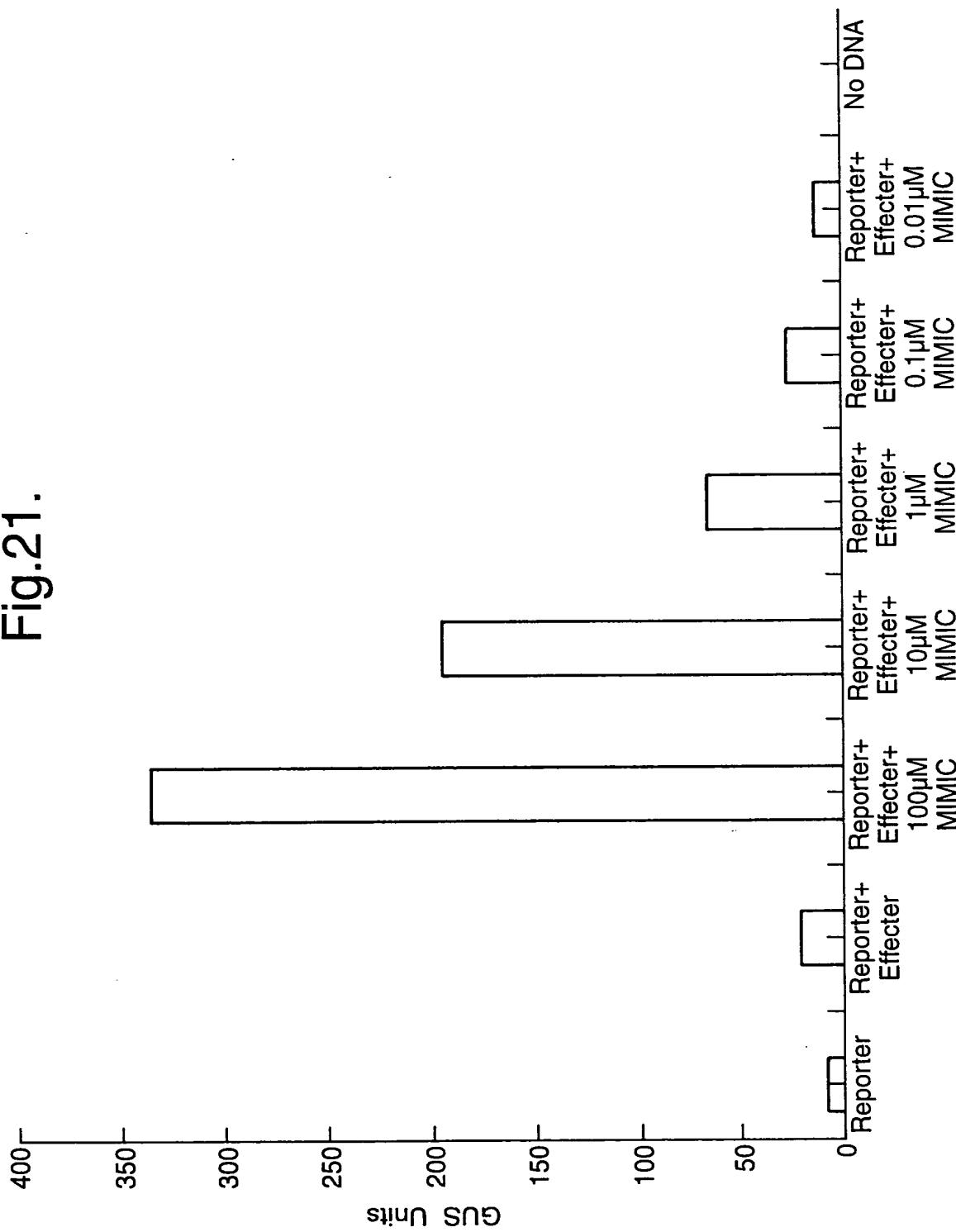


Fig.22.

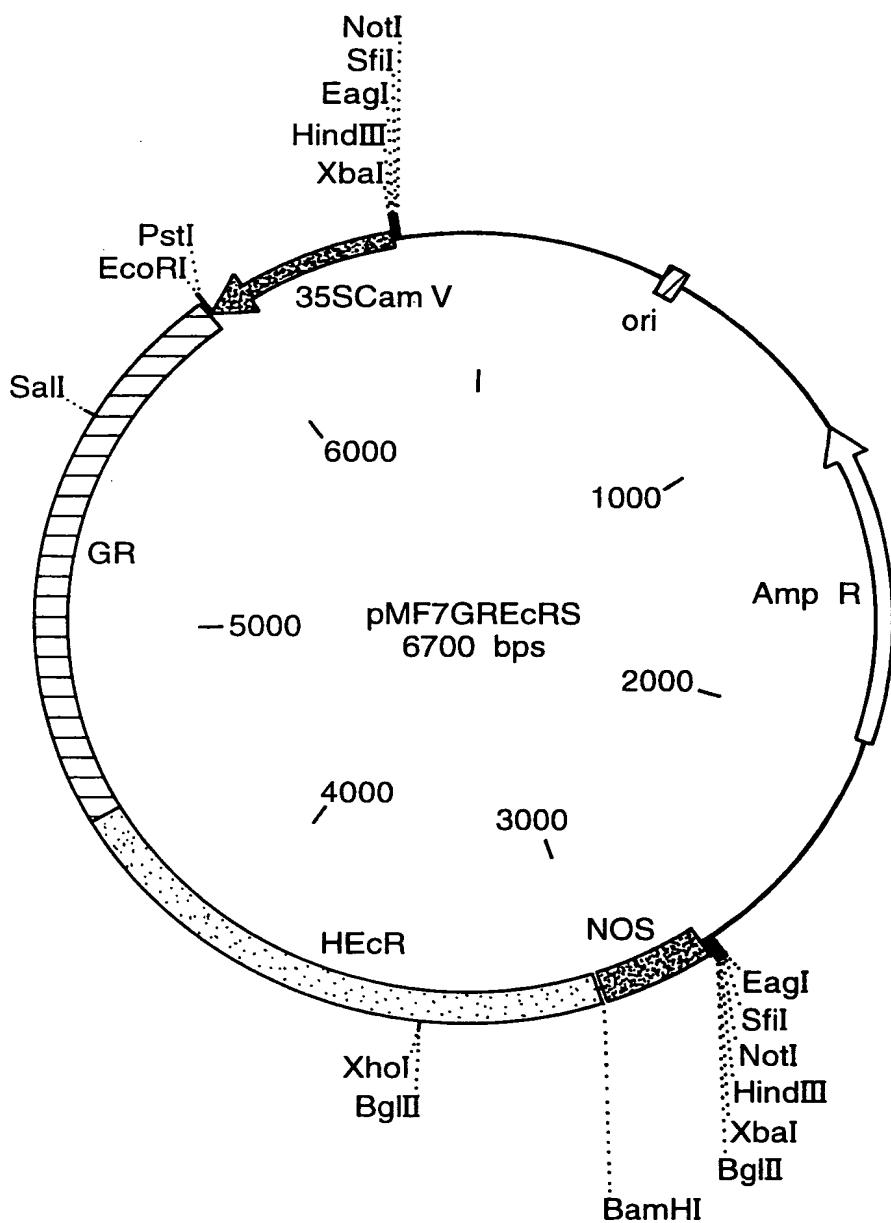


Fig.23.

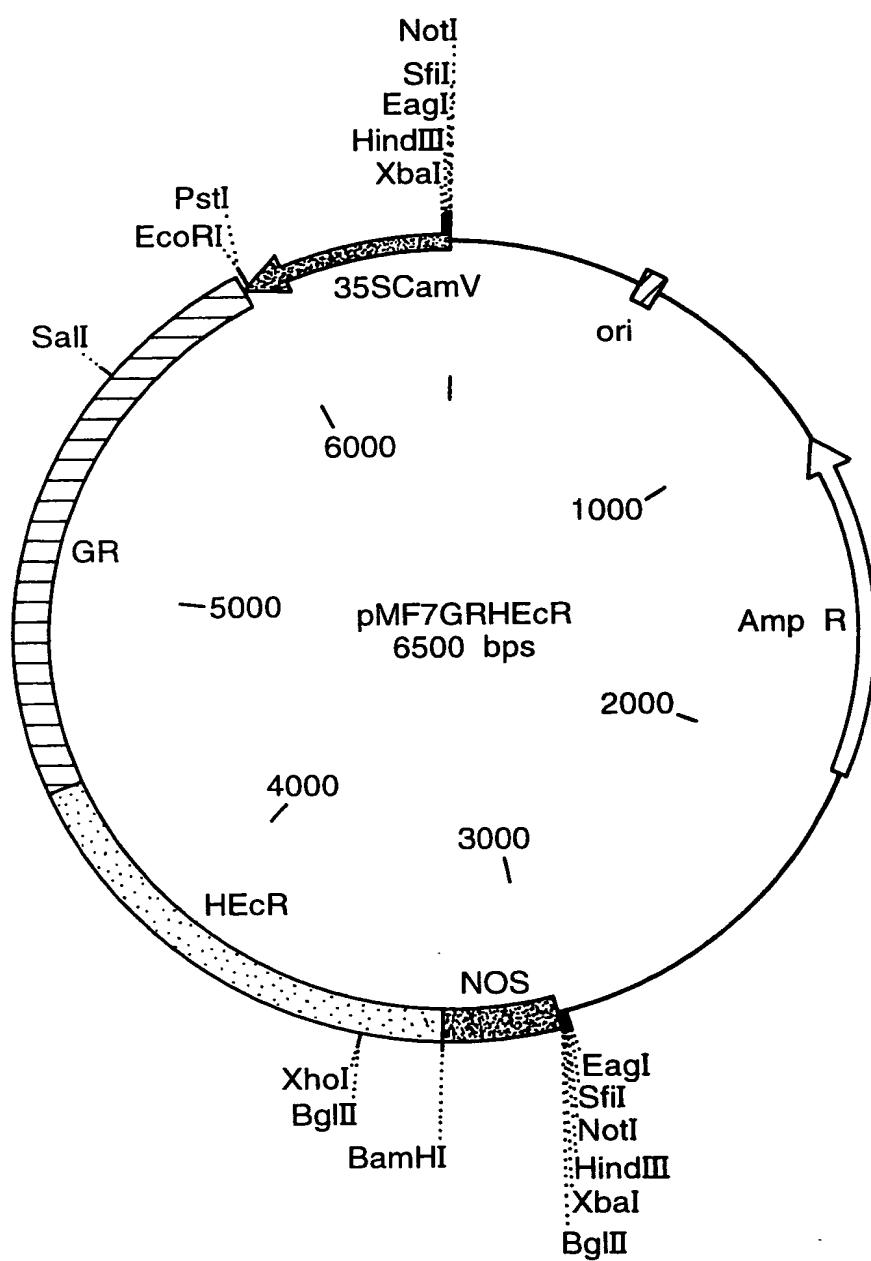


Fig.24.

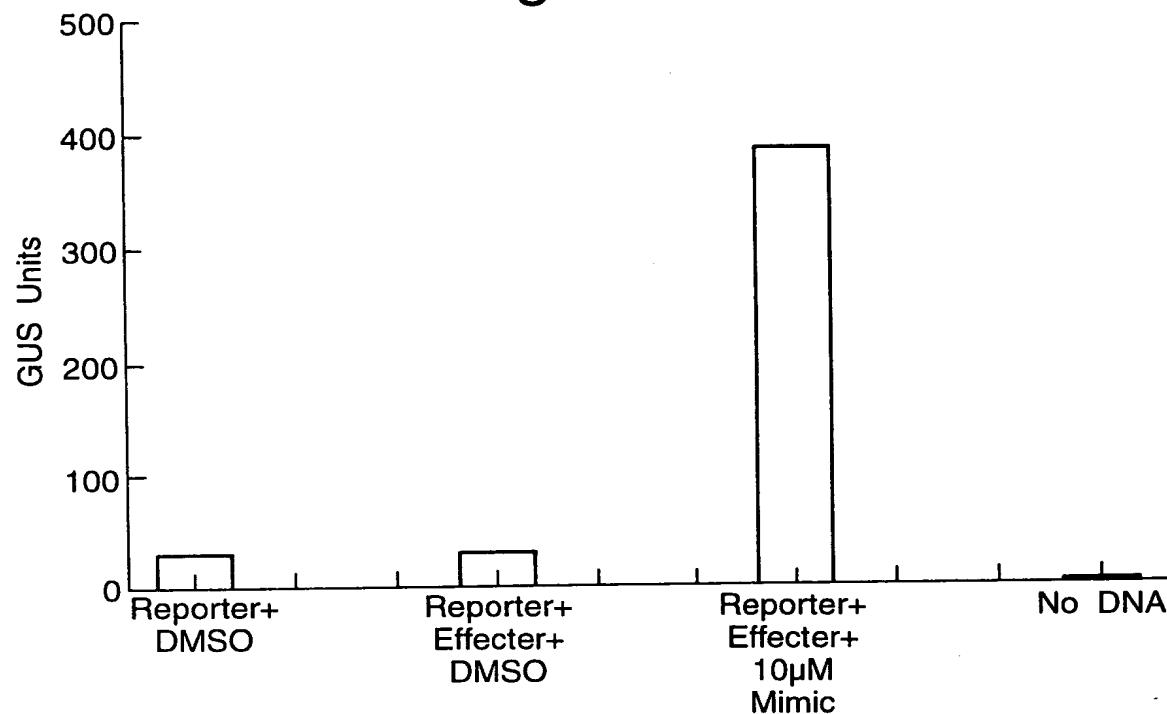


Fig.26.

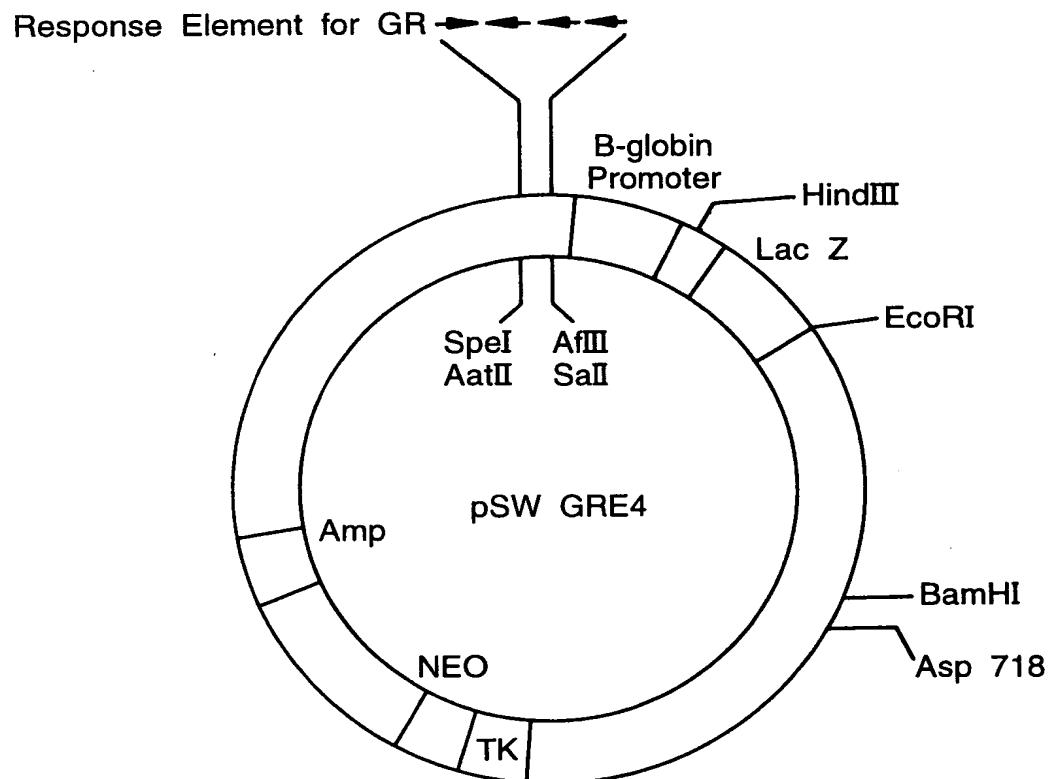


Fig.25.

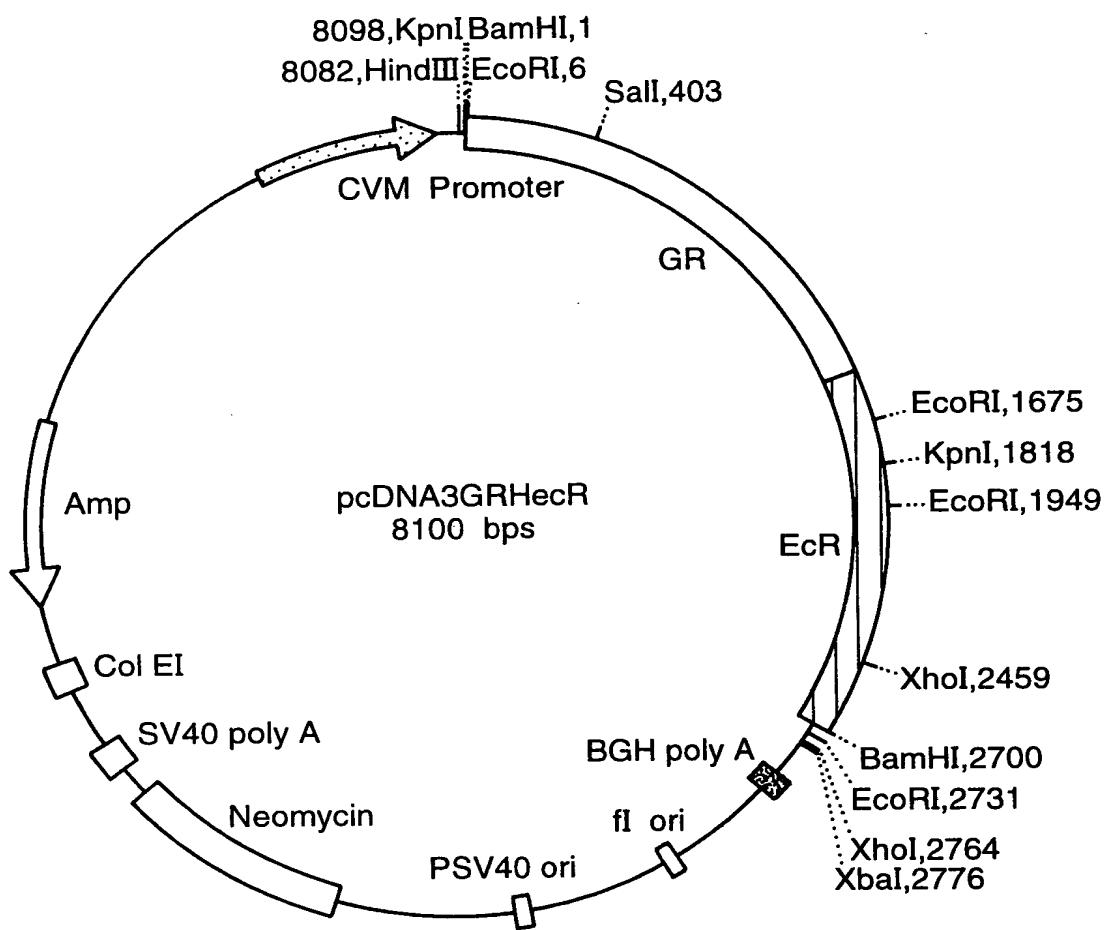


Fig.27.

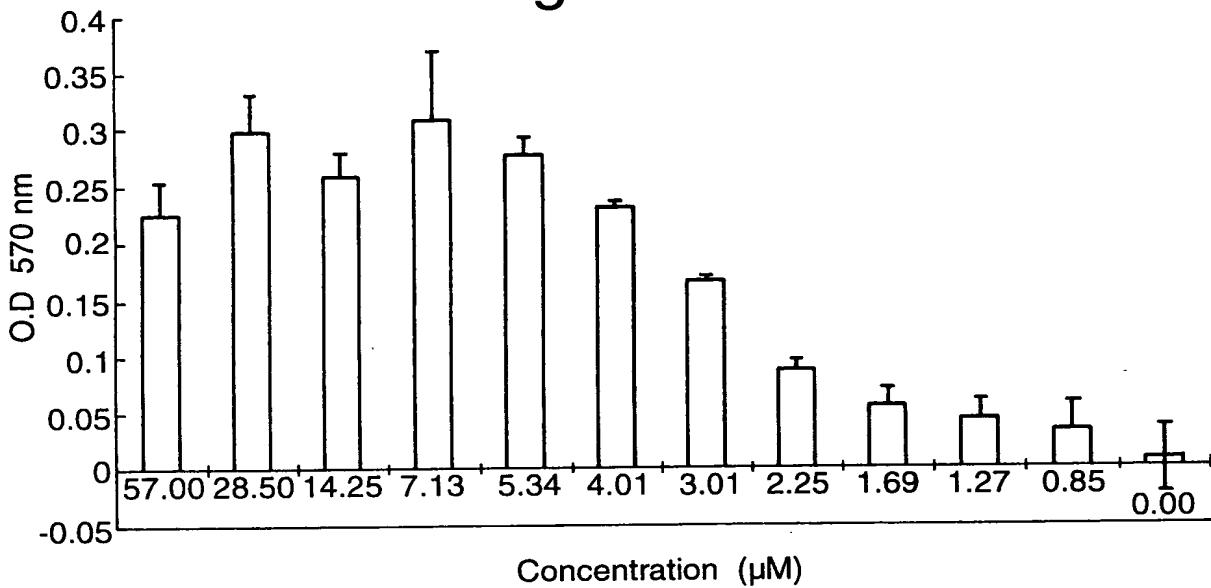


Fig.28.

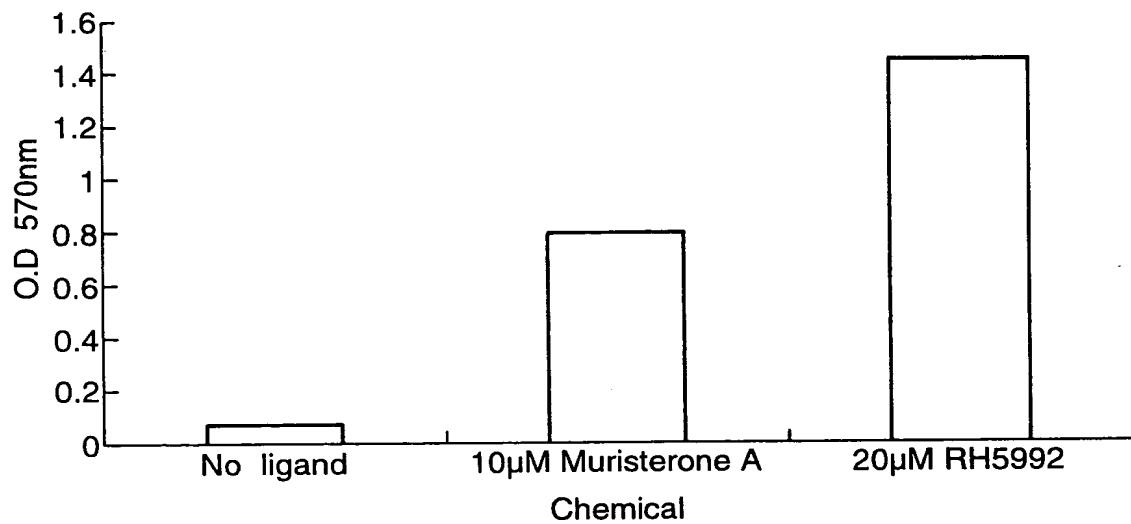


Fig.29.

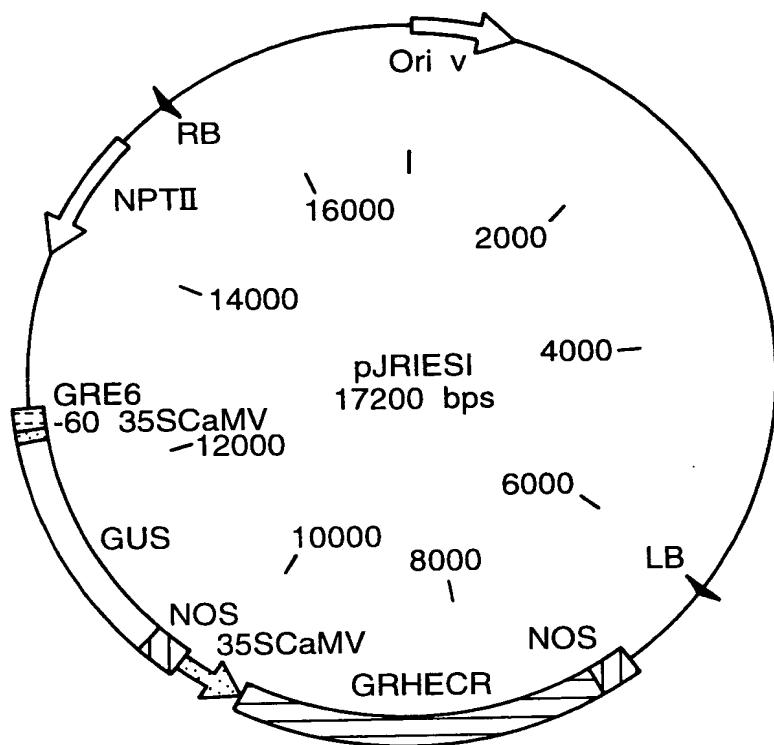


Fig.30.

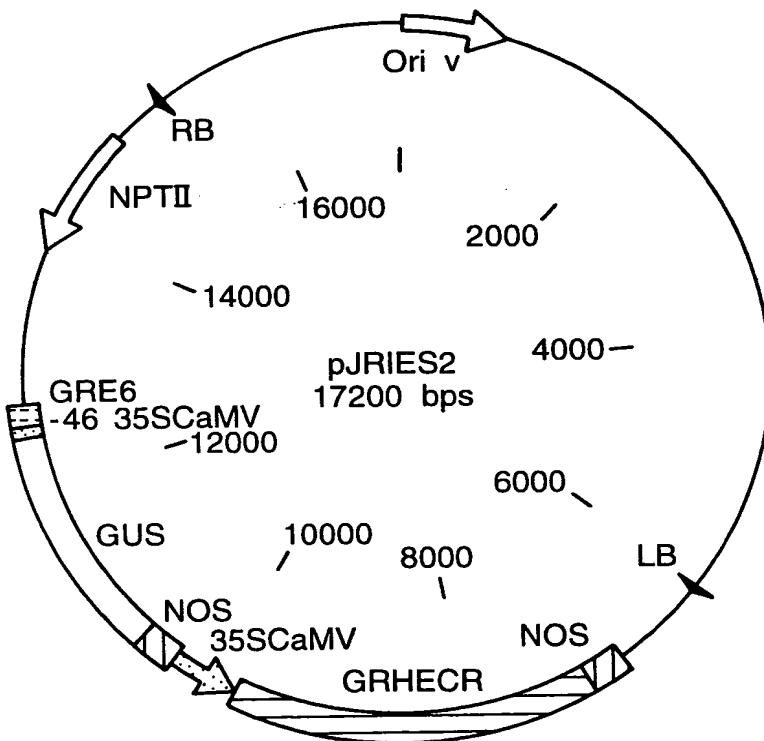


Fig.31.

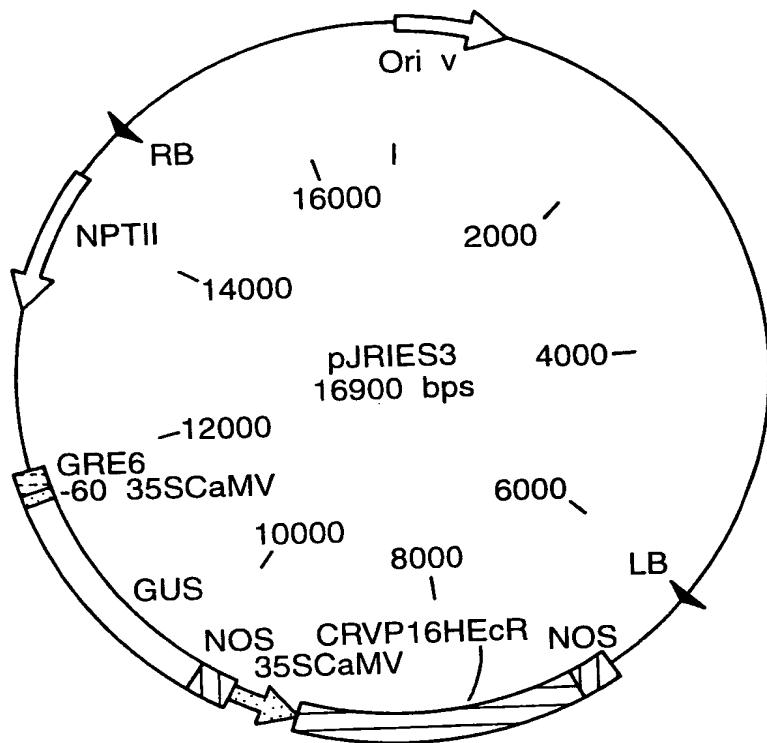


Fig.32.

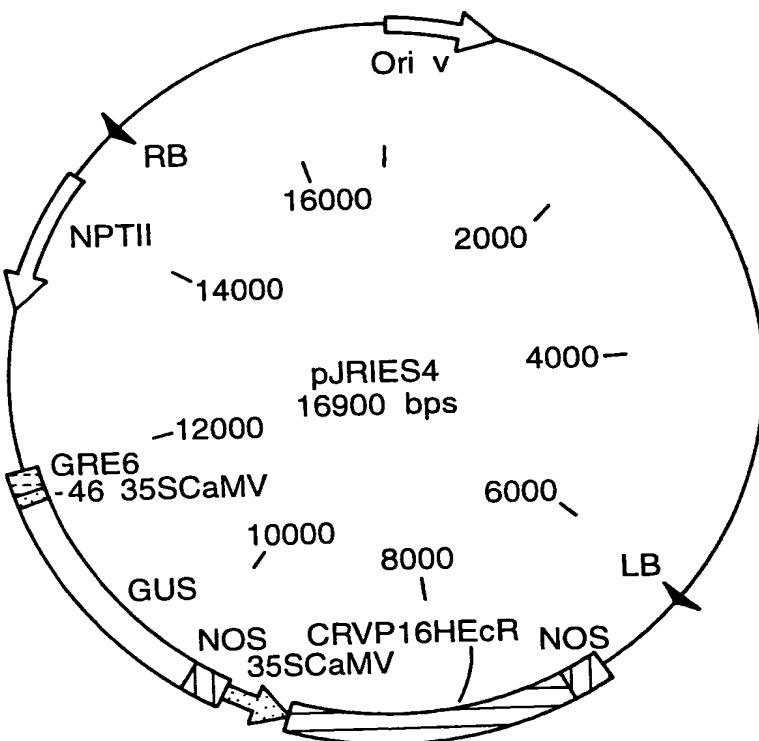


Fig.33.

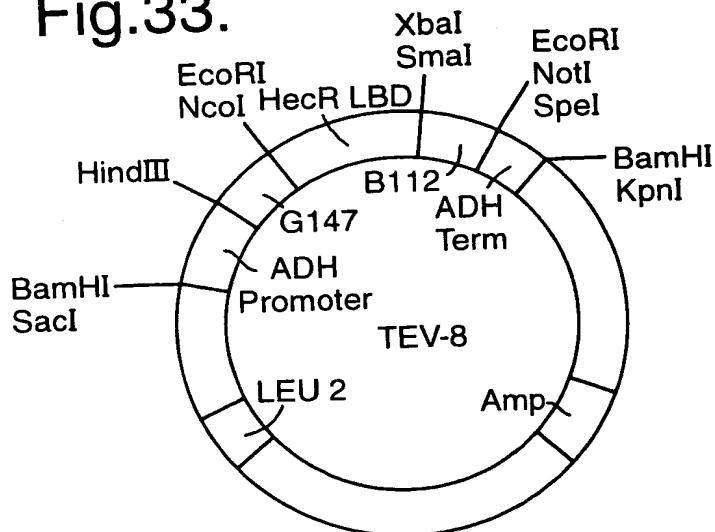


Fig.34.

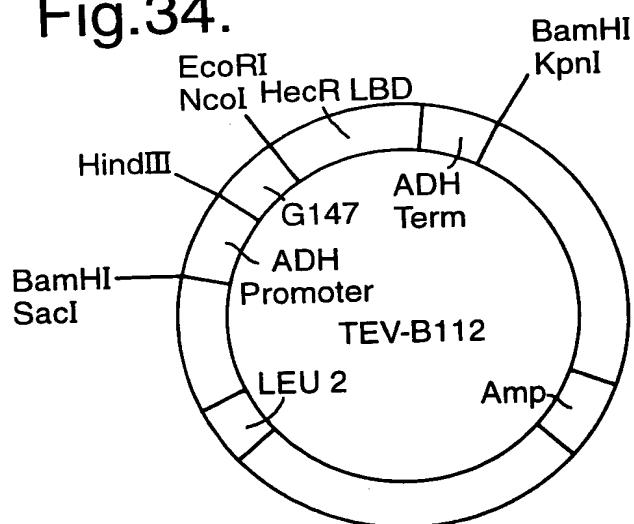


Fig.35.

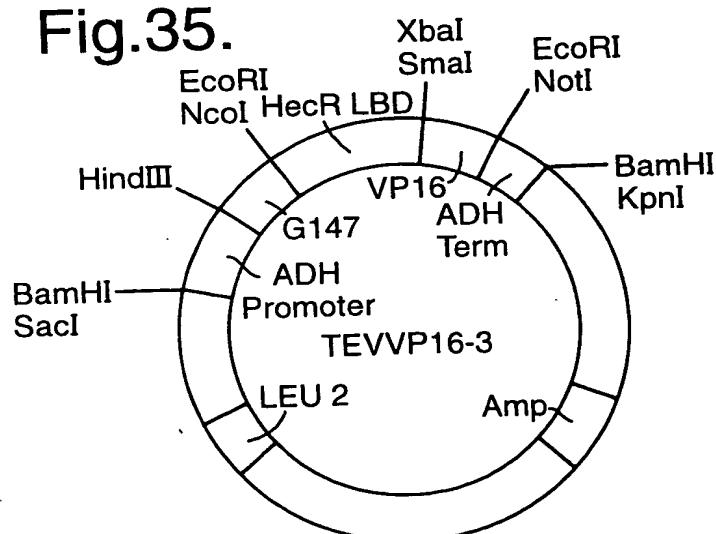


Fig.36.

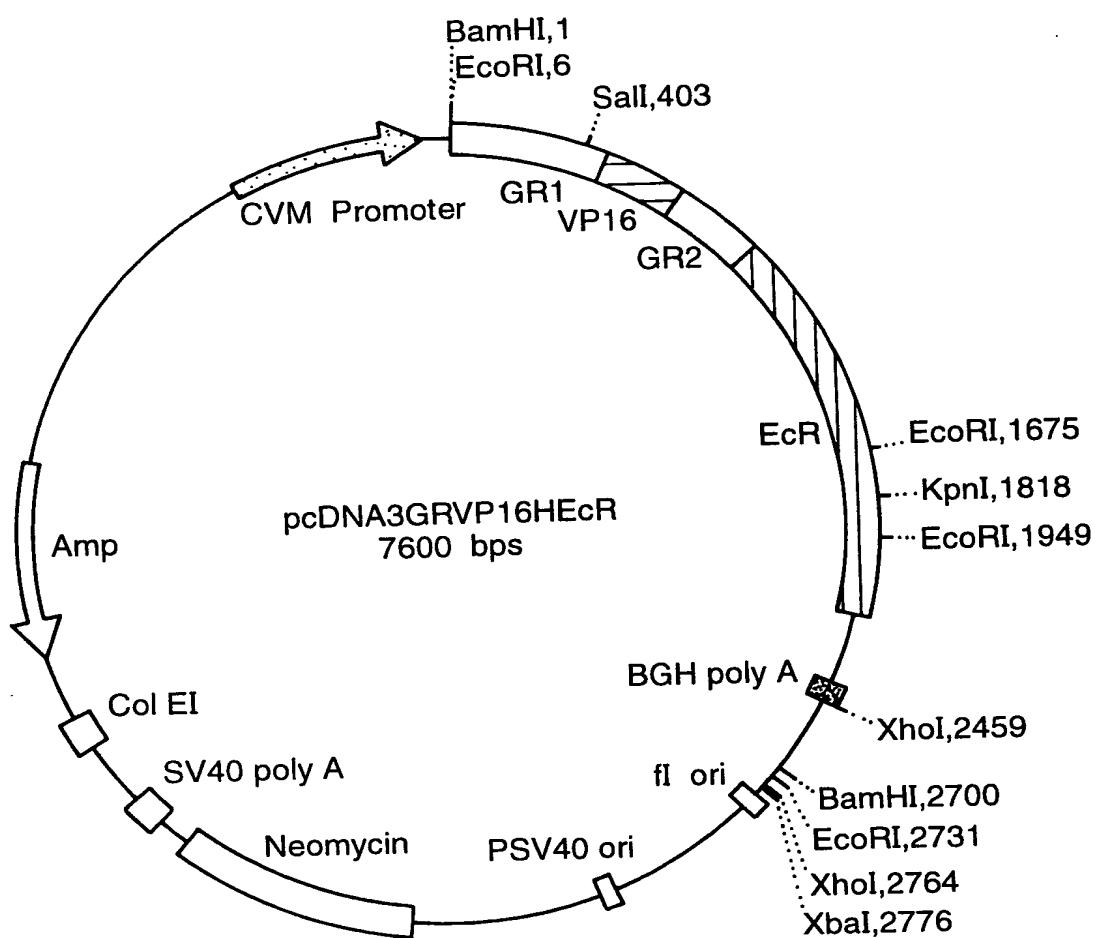


Fig.37.

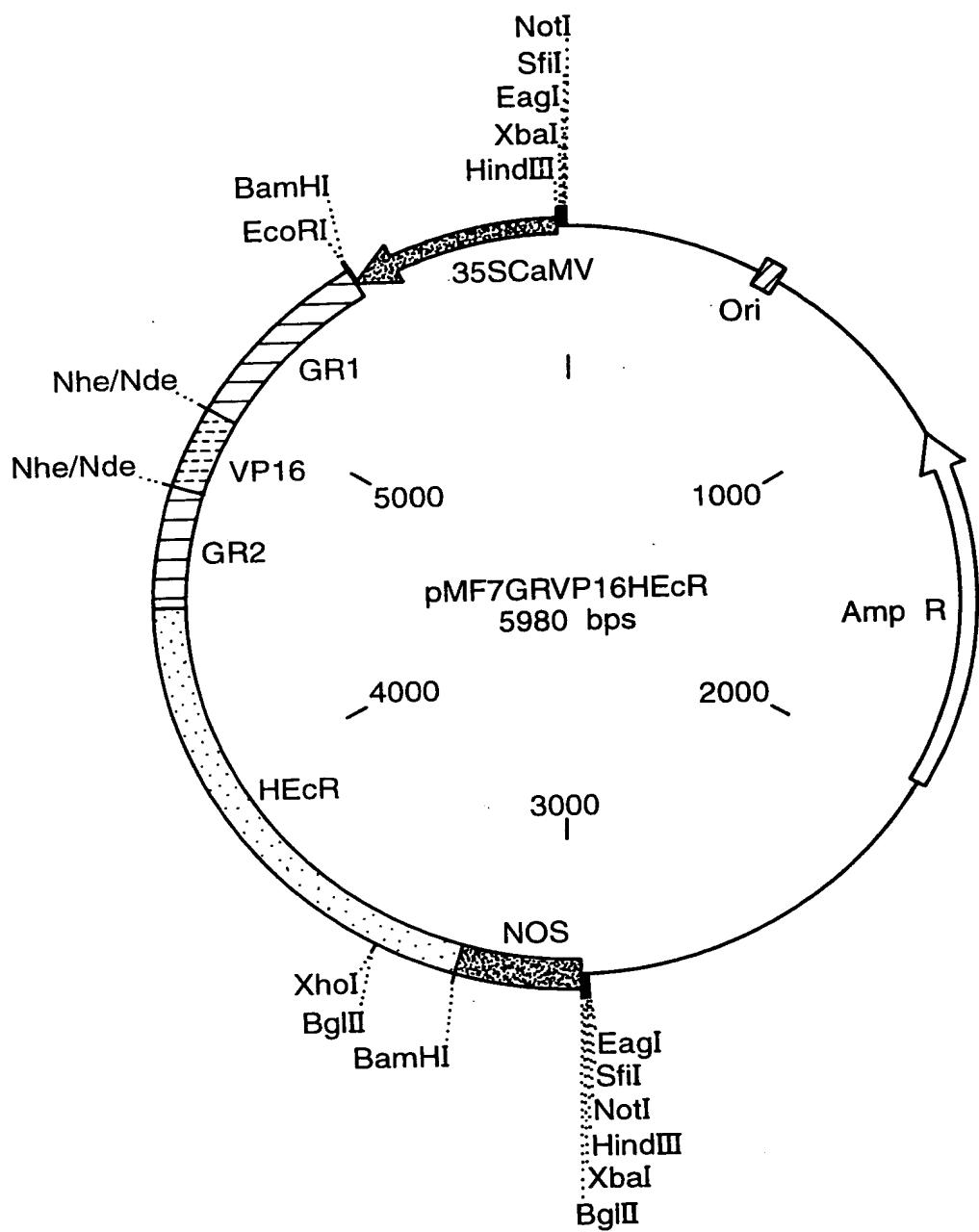
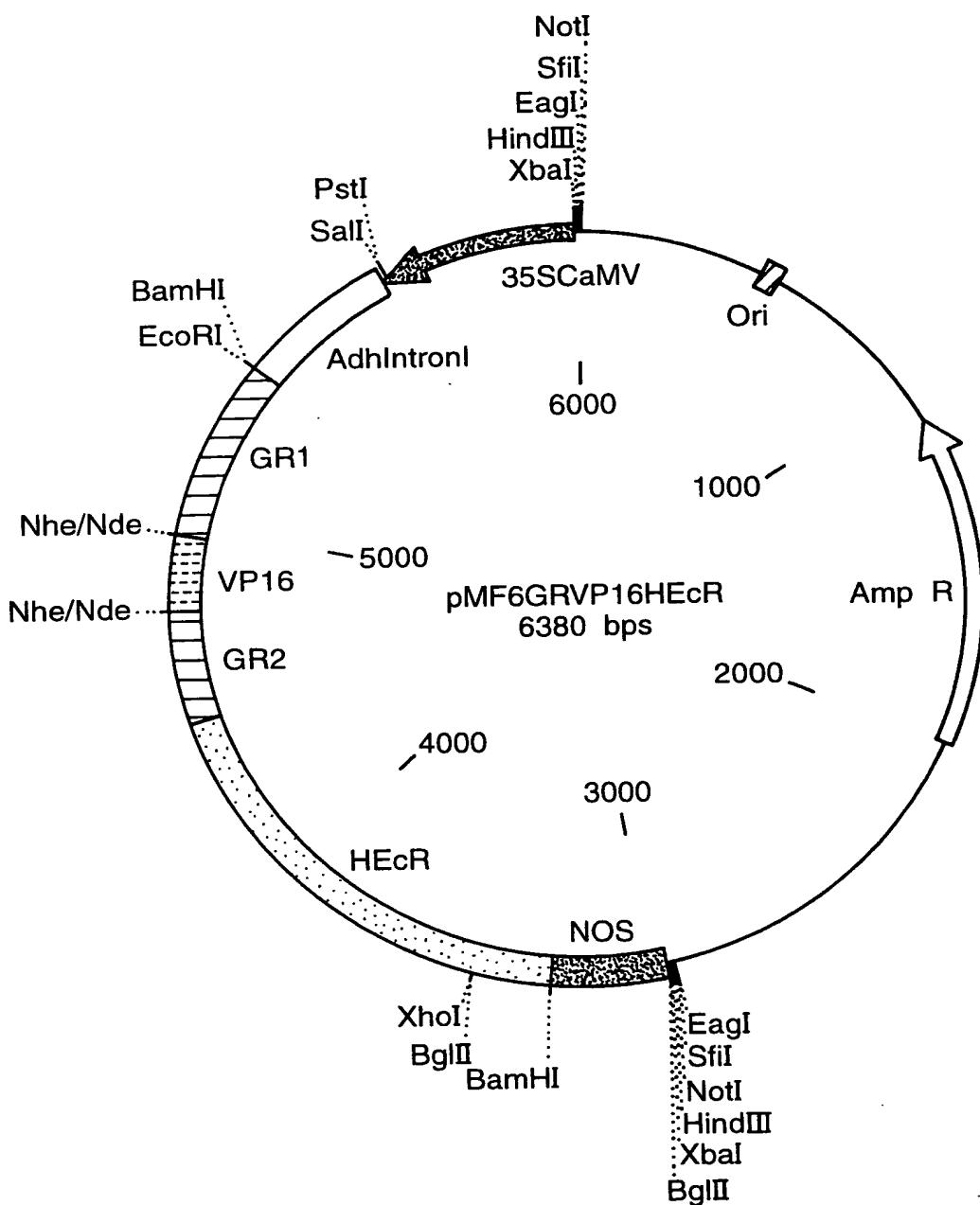
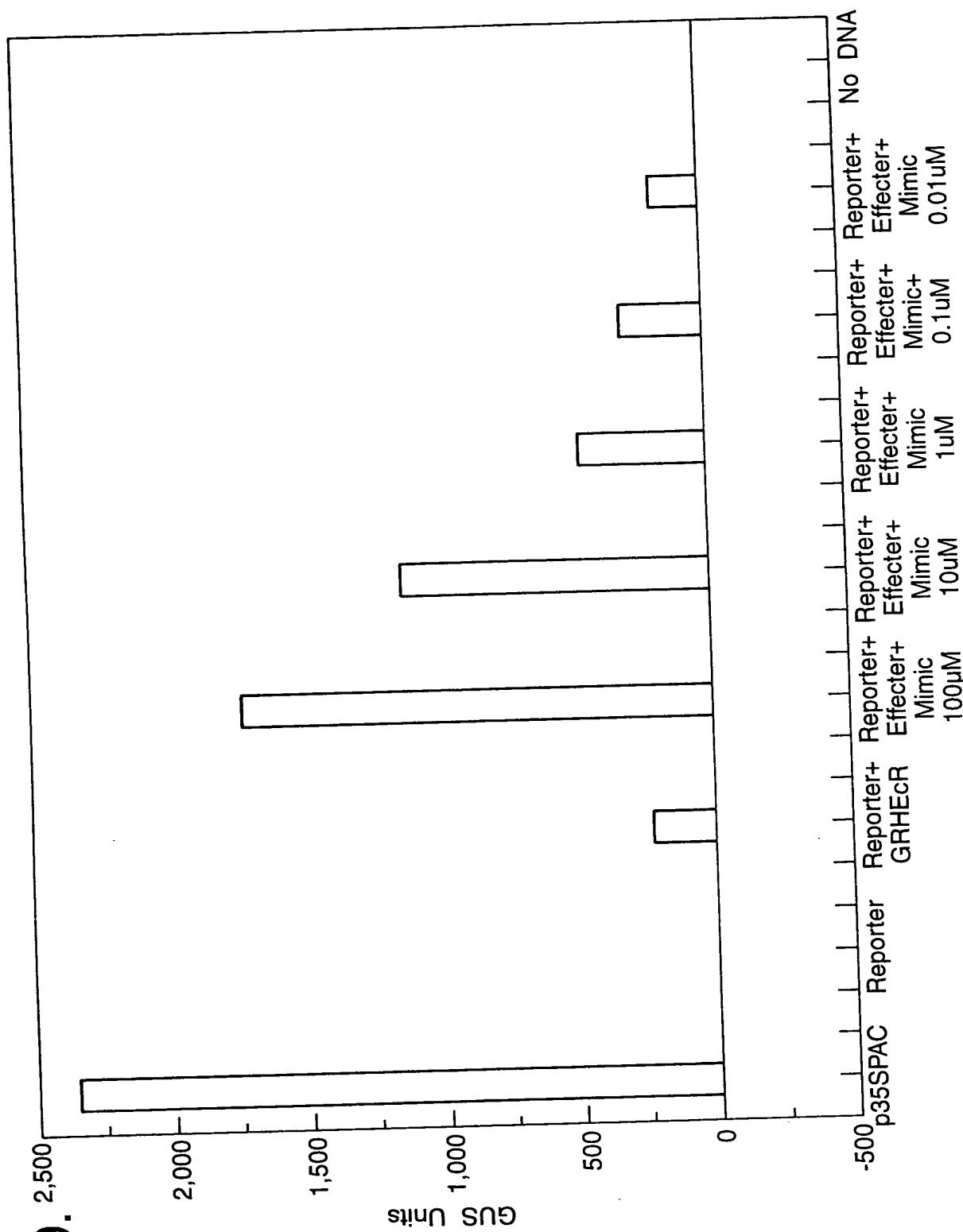


Fig.38.



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**Fig. 39.** 2,500

Spodoptera exigua DNA sequence.

Fig.40.

Sequence ID 6

SPODOPTERA EXIGUA HINGE AND LIGAND BINDING DOMAINS

3	9	15	21	27	33	39	45
1	AGG CCG GAG TGC GTG CCA GAA AAC CAG TGT GCA ATG AAA AGG						
TCC GGC CTC ACG CAC CAC GGT CTT TTG GTC ACA CGT TAC TTT TCC							
46 AAA GAG AAA AAG GCA CAA AGG GAA AAA GAC AAG TTG CCA GTC AGT							
TTT CTC TTC CGT GTT TCC CTT CCT TAC GGA GGG TAA TAC GTC ACA TCA							
91 ACA ACG ACA GTG GAT GAT CAC ATG CCT CCC ATT ATG CAG TGT GAT							
TGT TGC TGT CAC CTA CTA GTG TAC GGA GGG TAA TAC GTC ACA CTA							
136 CCA CCG CCT CCA GAG GCC GCA AGA ATT CAC GAG GTG GTG CCA CGA							
GGT GGC GGA GGT CTC CGG CGT TCT TAA GTG CTC CAC CAC GGT GCT							
181 TTC CTG AAT GAA AAG CTA ATG GAC AGG ACA AGG CTC AAG AAT GTG							
AAG GAC TTA CTT TTC GAT TAC CTG TCC TGT TCC GAG TTC TTA CAC							
226 CCC CCT CAC TGC CAA CCA GAA GTC CTT AAT AGC GAG GCT GGT CTG							
GGG GGA GTG AC GGT CTT GGT CTT CAG GAA TTA TCG CTC CGA CCA GAC							
271 GTA CCA AGA AGG CTA TGA ACA GCC ATC AGA AGA GGA TCT AAA AAG							
CAT GGT TCT TCC GAT ACT TGT CGG TAG TCT CCT AGA TTT TTC							

**Fig.40 i.**

316 AGT CAC ACA GTC GGA TGA AGA CGA AGA GTC GGA CAT GCC GTT  
TCA GTG TGT CAG CCT ACT TCT GCT TCT CAG CCT GTA CGG CAA

361 CCG TCA GAT CAC CGA GAT GAC CCT CAC AGT GCA GCT CAT TGT  
GGC AGT CTA GTG GCT CTA CTG CTA GGA GTG TCA CGT CGA GTA ACA

406 TGA ATT CGC TAA GGG CCT ACC AGC GTT CGC AAA GAT CTC ACA GTC  
ACT TAA GCG ATT CCC GGA TGG TCG CAA GCG TTT CTA GAG TGT CAG

451 GGA TCA GAT CAC ATT ATT AAA GGC CTG TTC GAG TGA GGT GAT GAT  
CCT AGT CTA GTG TAA TAA ATT CCG GAC AAG CTC ACT CCA CTA CTA

496 GTT GCG AGT AGC TCG GCG GTA CGA CGC GGC GAC AGA CAG CGT GTT  
CAA CGC TCA TCG AGC CGC CAT GCT GCG CCG CTG TCT GTC GCA CAA

541 GTT CGC CAA CCA CCA GGC GTA CAC CCG CGA CAA CTA CCG CAA GGC  
CAA CGG GTT GGT CGG CAT GTG GGC GCT GTT GAT GGC GTT CGG

586 AGG CAT GGC CTA CGT CAT CGA GGA CCT GCT GCA CTT CTG CCG GTG  
TCC GTA CCG GAT GCA GTA GCT CCT CGA CGT GAA GAC GGC CAC

631 CAT GTA CTC CAT GAT GGA TAA CGT CCA CTA TGC ACT GCT CAC  
GTA CAT GAG GTA CTA CTC CCT ATT GCA GGT GAT ACG TGA CGA GTG

676 TGC CAT CGT CAT TTT CTC AGA CCG ACC CGG GCT TGA GCT AAC CCT  
ACG GTA GCA GTA AAA GAG TCT GGC TGG GCC CGA ACT CGA TTG GGA

721 GTT GGT GGA GAT CCA GAG ATA TTA CCT GAA CAC GCT GCG GGT  
CAA CCA CCT CTA GGT CTC TAT ATT GGA CTT GTG CGA CGC CCA

Title: METHOD FOR CONTROLLING  
GENE EXPRESSION IN A CELL  
Inventor: Jepson et al.  
Atty Docket: 1392/4/3/2

Fig.40 ii. 766 GTA CAT CCT GAA CCA GAA CAG TCG GTC GCC GTG CCC TGT CAT  
CAT GGA CTT GGT CCT GTC AGC CAG CGG CAC GAC GGG ACA GTA  
  
811 CTA CGC TAA GAT CCT CGG CAT CCT GAC GGA GCT GCG GAC CCT GGG  
GAT GCG ATT CTA GGA GCC GTA GGA CTG CCT CGA CGC CTG GGA CCC  
  
856 CAT GCA GAA CTC CAA CAT GTG CAT CTC ACT CAA GCT GAA GAA CAG  
GTA CGT CTT GAG GTT GTA CAC GTA GAG TGA GTT CGA CTT CTT GTC  
  
901 GAA CGT GCC GCC GTT CTT CGA GGA TAT CTG GGA CGT CCT CGA GCT CAT  
CTT GCA CGG CGG CAA GAA CCT CCT ATA GAC CCT GCA GGA GCT CAT  
  
946 AAA  
TTT

Total number of bases is: 948.

Sequence I.D. 7

Fig.41.

Sequence comparison between *Heliothis 19R* clone and *secr* *Taq* clone

Title: METHOD FOR CONTROLLING  
GENE EXPRESSION IN A CELL

Inventor: Jepson et al.  
Atty Docket: 1392/4/3/2

HECR	RPECVVPENQCAMKRKEKKAQREKD <b>KL</b> PVSTTTVDDHMPPIMQCDPPPPEAARILECVQ
SECR	RPECVVPENQCAMKRKEKKAQREKD <b>KL</b> PVSTTTVDDHMPPIMQCDPPPPEAARI
HECR	HEVVPRFLNEKLMEQNRLKVNVEPPLTANQKS <b>L</b> IARLVWYQEGYEQPSEEDLKRV <b>T</b> QSD
SECR	HEVVPRFLNEKLMERTRL <b>R</b> NVVEPPLTANQKS <b>L</b> IARLVWYQEGYEQPSEEDLKRV <b>T</b> QSD
HECR	EDDEDSDMPPFRQITEMTILTQVLIVEFAKGLP <b>G</b> FAKISQSDQIT <b>I</b> LLKACSSSEVMMLR
SECR	EDEEESDMPPFRQITEMTILTQVLIVEFAKGLP <b>A</b> FAKISQSDQIT <b>I</b> LLKACSSSEVMMLR
HECR	VARRYDAATDSVLFANNQAYTRDNYRKAGMAYVIEDL <b>L</b> HFCRCMYSMMMDNVHYALL
SECR	VARRYDAATDSVLFANNQAYTRDNYRKAGMAYVIEDL <b>L</b> HFCRCMYSMMMDNVHYALL
HECR	TAIVIFSDRPGLEQPLVVEI <b>Q</b> RYYLNTLRVYILNQNNSASPRGAVIFGEILGILTEI
SECR	TAIVIFSDRPGLELTLLVEI <b>Q</b> RYYLNTLRVYILNQNNSRSPCCPVI <b>Y</b> AKILGILTEI
HECR	RTLGMQNSNM <b>C</b> ISLKLKKRKLPPFFLEIDWDV
SECR	RTLGMQNSNM <b>C</b> ISLKLKNRNVPFFEDIDWDV

Fig.42.

